

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: CREATOGEN Biosciences GmbH  
 (B) STREET: Ulmer Strasse 160 a  
 (C) CITY: Augsburg  
 (E) COUNTRY: DE  
 (F) POSTAL CODE (ZIP): 86156

(A) NAME: Max-Planck-Gesellschaft zur Foerderung der  
 Wissenschaften e.V.  
 (B) STREET: Hofgartenstrasse 2  
 (C) CITY: Muenchen  
 (E) COUNTRY: DE  
 (F) POSTAL CODE (ZIP): 80539

(ii) TITLE OF INVENTION: Helicobacter proteins for  
 identification, development and optimisation of  
 immunological and pharmacological active ingredients

(iii) NUMBER OF SEQUENCES: 114

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 873 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS001 (HPS166)

## (ix) FEATURES:

(A) NAME/KEY: CDS  
 (B) POSITION:1..873

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG AAA TTT TTA CGC TCT GTT TAT GCA TTT TGC TCC AGT TGG GTA GGG	48
Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser Ser Trp Val Gly	
1 5 10 15	
ACG ATT GTT ATT GTG CTG TTG GTT ATC TTT TTT ATC GCG CAA GCC TTT	96
Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile Ala Gln Ala Phe	
20 25 30	
ATC ATT CCC TCT CGC TCT ATG GTT GGC ACG CTC TAT GAG GGC GAC ATG ....	144

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Ile	Ile	Pro	Ser	Arg	Ser	Met	Val	Gly	Thr	Leu	Tyr	Glu	Gly	Asp	Met	
		35					40					45				
CTC	TTT	GTC	AAA	AAG	TTT	TCT	TAC	GGC	ATA	CCC	ATT	CCT	AAA	ATC	CCA	192
Leu	Phe	Val	Lys	Lys	Phe	Ser	Tyr	Gly	Ile	Pro	Ile	Pro	Lys	Ile	Pro	
	50					55				60						
TGG	ATT	GAG	CTT	CCT	GTT	ATG	CCT	GAT	TTT	AAA	AAT	AAC	GGA	CAT	TTG	240
Trp	Ile	Glu	Leu	Pro	Val	Met	Pro	Asp	Phe	Lys	Asn	Asn	Gly	His	Leu	
	65				70				75						80	
ATA	GAG	GGG	GAT	CGC	CCT	AAG	CGT	GGC	GAA	GTG	GTG	GTG	TTT	ATC	CCT	288
Ile	Glu	Gly	Asp	Arg	Pro	Lys	Arg	Gly	Glu	Val	Val	Val	Phe	Ile	Pro	
				85				90						95		
CCC	CAT	GAA	AAA	AAG	TCT	TAC	TAT	GTT	AAA	AGG	AAT	TTT	GCC	ATT	GGA	336
Pro	His	Glu	Lys	Lys	Ser	Tyr	Tyr	Val	Lys	Arg	Asn	Phe	Ala	Ile	Gly	
			100					105					110			
GGC	GAT	GAG	GTG	TTG	TTC	ACT	AAT	GAG	GGT	TTT	TAT	TTG	CAC	CCT	TTT	384
Gly	Asp	Glu	Val	Leu	Phe	Thr	Asn	Glu	Gly	Phe	Tyr	Leu	His	Pro	Phe	
		115					120					125				
GAG	AGC	GAC	ACG	GAC	AAA	AAT	TAC	ATC	GCT	AAA	CAT	TAC	CCT	AAC	GCC	432
Glu	Ser	Asp	Thr	Asp	Lys	Asn	Tyr	Ile	Ala	Lys	His	Tyr	Pro	Asn	Ala	
	130					135					140					
ATG	ACA	AAA	GAA	TTT	ATG	GGT	AAA	ATT	TTT	GTT	TTA	AAC	CCT	TAT	AAA	480
Met	Thr	Lys	Glu	Phe	Met	Gly	Lys	Ile	Phe	Val	Leu	Asn	Pro	Tyr	Lys	
	145				150				155						160	
AAT	GAG	CAT	CCG	GGT	ATC	CAT	TAC	CAA	AAA	GAC	AAT	GAA	ACC	TTC	CAC	528
Asn	Glu	His	Pro	Gly	Ile	His	Tyr	Gln	Lys	Asp	Asn	Glu	Thr	Phe	His	
				165				170						175		
TTA	ATG	GAG	CAA	TTA	GCC	ACT	CAA	GGC	GCA	GAA	GCT	AAT	ATC	AGC	ATG	576
Leu	Met	Glu	Gln	Leu	Ala	Thr	Gln	Gly	Ala	Glu	Ala	Asn	Ile	Ser	Met	
			180				185						190			
CAA	CTC	ATT	CAA	ATG	GAG	GGC	GAA	AAG	GTG	TTT	TAT	AAG	AAA	ATC	AAT	624
Gln	Leu	Ile	Gln	Met	Glu	Gly	Glu	Lys	Val	Phe	Tyr	Lys	Lys	Ile	Asn	
		195				200						205				
GAC	GAT	GAA	TTT	TTC	ATG	ATC	GGC	GAC	AAC	AGA	GAC	AAT	TCT	AGC	GAC	672
Asp	Asp	Glu	Phe	Phe	Met	Ile	Gly	Asp	Asn	Arg	Asp	Asn	Ser	Ser	Asp	
	210					215					220					
TCG	CGC	TTT	TGG	GGG	AGT	GTG	GCT	TAT	AAA	AAC	ATC	GTG	GGT	TCG	CCA	720
Ser	Arg	Phe	Trp	Gly	Ser	Val	Ala	Tyr	Lys	Asn	Ile	Val	Gly	Ser	Pro	
	225				230				235						240	
TGG	TTT	GTT	TAT	TTC	AGT	TTG	AGT	TTA	AAA	AAT	AGC	CTA	GAA	ATG	GAT	768
Trp	Phe	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Lys	Asn	Ser	Leu	Glu	Met	Asp	
				245				250						255		
GCA	GAA	AAT	AAC	CCT	AAA	AAA	CGC	TAT	CTG	GTG	CGT	TGG	GAA	CGC	ATG	816
Ala	Glu	Asn	Asn	Pro	Lys	Lys	Arg	Tyr	Leu	Val	Arg	Trp	Glu	Arg	Met	
			260					265					270			

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TTT AAA AGC GTT GGA GGC TTA GAA AAA ATC ATT AAA AAA GAA AAC GCA 864  
 Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys Lys Glu Asn Ala  
           275                          280                          285

ACG CAT TAA 873  
 Thr His \*  
           290

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 291 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser Ser Trp Val Gly  
   1                          5                          10                          15  
 Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile Ala Gln Ala Phe  
           20                          25                          30  
 Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu Gly Asp Met  
           35                          40                          45  
 Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro  
           50                          55                          60  
 Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu  
           65                          70                          75                          80  
 Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro  
                           85                          90                          95  
 Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly  
           100                          105                          110  
 Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe  
           115                          120                          125  
 Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr Pro Asn Ala  
           130                          135                          140  
 Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn Pro Tyr Lys  
           145                          150                          155                          160  
 Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu Thr Phe His  
           165                          170                          175  
 Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn Ile Ser Met  
           180                          185                          190  
 Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys Lys Ile Asn  
           195                          200                          205  
 Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn Ser Ser Asp

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375

380

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu Thr Tyr Lys Ile Thr
 1             5             10             15
Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly Leu Val Val Gly Leu
          20             25             30
Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu
          35             40             45
Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr
          50             55             60
Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile
65             70             75             80
Lys Leu Ile Pro Lys Ile Ile Gly *
          85

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## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPC005

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..714

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

ATG CCT ATT AAC CCT CTC TAT CTT TTC CCT AAT CTT TTT ACC GCT AGC      48
Met Pro Ile Asn Pro Leu Tyr Leu Phe Pro Asn Leu Phe Thr Ala Ser
 90             95             100             105

AGT ATT TTT TTA GGC ATG ATG AGT ATT TTT TAC GCT TCC AGT TAC CAA      96
Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala Ser Ser Tyr Gln
          110             115             120

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 238 Amino acids  
(B) TYPE: Amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Pro Ile Asn Pro Leu Tyr Leu Phe Pro Asn Leu Phe Thr Ala Ser  
1 5 10 15  
Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala Ser Ser Tyr Gln  
20 25 30  
Phe Val Met Ala Cys Trp Leu Val Val Ala Ser Leu Ile Leu Asp Gly  
35 40 45  
Leu Asp Gly Arg Val Ala Arg Leu Thr Asn Thr Thr Ser Lys Phe Gly  
50 55 60  
Ile Glu Phe Asp Ser Leu Ala Asp Val Ile Ala Phe Gly Val Ala Pro  
65 70 75 80  
Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe Gly Arg Ile Gly  
85 90 95  
Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala Ile Arg Leu Ala  
100 105 110  
Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr Ser Phe Ile Gly  
115 120 125  
Ile Pro Ile Pro Ala Ala Ala Val Leu Val Val Leu Cys Val Leu Leu  
130 135 140  
Asp Asn Lys Tyr His Phe Leu Glu Gly Asn Thr Glu Lys Leu Phe Leu  
145 150 155 160  
Ser Phe Ile Val Leu Leu Gly Val Leu Met Val Ser Asn Ile Arg Tyr  
165 170 175  
Pro Asn Phe Lys Lys Val Lys Trp Asn Leu Lys Leu Phe Ile Leu Val  
180 185 190  
Leu Ile Phe Leu Ser Leu Val Phe Val Arg Pro Leu Glu Ala Leu Ser  
195 200 205  
Val Phe Met Gly Leu Tyr Leu Ile Tyr Gly Ile Ile Arg Trp Leu Phe  
210 215 220  
Leu Met Val Lys Ile Ile Phe Asn Lys Asn Lys Ser Ala \*  
225 230 235

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

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D

(vii) DIRECT SOURCE:

(B) CLONE(S): HPC029 (HPC030)

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) POSITION:1..552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GCA GAA GAA CAA GAA AAT ACC GCG CAA CAA CCC CAA AAA AAA AGC	48
Met Ala Glu Glu Gln Glu Asn Thr Ala Gln Gln Pro Gln Lys Lys Ser	
240 245 250	
AAA GCC CTT TTA TTT GTC ATT ATT GGA AGC GTG TTA GTG ATG CTT TTG	96
Lys Ala Leu Leu Phe Val Ile Ile Gly Ser Val Leu Val Met Leu Leu	
255 260 265 270	
TTG GTG GGG GTG ATT ATC ATG CTG CTT ATG GGG AAT AAG GAA GAA TCC	144
Leu Val Gly Val Ile Ile Met Leu Leu Met Gly Asn Lys Glu Glu Ser	
275 280 285	
AAA GAA AAC GCT TCT AAA AAC ACC CAA GAA GTC CAA GCT AAT CCT ATG	192
Lys Glu Asn Ala Ser Lys Asn Thr Gln Glu Val Gln Ala Asn Pro Met	
290 295 300	
GCG AAC AAA AAT CAA GAA GCC AAA GAA GGC TCT AAT ATC CAG CAA TAT	240
Ala Asn Lys Asn Gln Glu Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr	
305 310 315	
CTG GTG CTT GGG CCT TTG TAT GCG ATT GAT GCG CCT TTT GCG GTG AAT	288
Leu Val Leu Gly Pro Leu Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn	
320 325 330	
TTG GTT TCT CAA AAT GGC AGA CGC TAC CTT AAG GCT TCC ATT TCG TTA	336
Leu Val Ser Gln Asn Gly Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu	
335 340 345 350	
GAA TTG AGC AAT GAA AAG CTT TTA AAT GAA GTC AAG GTT AAA GAC ACA	384
Glu Leu Ser Asn Glu Lys Leu Leu Asn Glu Val Lys Val Lys Asp Thr	
355 360 365	
GCG ATT AAG GAC ACG ATT ATA GAG ATT CTA TCG TCT AAA AGC GTG GAA	432
Ala Ile Lys Asp Thr Ile Ile Glu Ile Leu Ser Ser Lys Ser Val Glu	
370 375 380	
GAA GTG GTT ACT AAC AAA GGT AAA AAC AAG CTT AAA GAT GAA ATT AAG	480
Glu Val Val Thr Asn Lys Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys	
385 390 395	
AGC CAT TTG AAT TCG TTT TTG ATT GAT GGC TTT ATT AAA AAT GTC TTT	528
Ser His Leu Asn Ser Phe Leu Ile Asp Gly Phe Ile Lys Asn Val Phe	
400 405 410	
TTC ACT GAT TTC ATT ATT CAA TAA	552
Phe Thr Asp Phe Ile Ile Gln *	
415 420	

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## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Glu Glu Gln Glu Asn Thr Ala Gln Gln Pro Gln Lys Lys Ser  
 1 5 10 15

Lys Ala Leu Leu Phe Val Ile Ile Gly Ser Val Leu Val Met Leu Leu  
 20 25 30

Leu Val Gly Val Ile Ile Met Leu Leu Met Gly Asn Lys Glu Glu Ser  
 35 40 45

Lys Glu Asn Ala Ser Lys Asn Thr Gln Glu Val Gln Ala Asn Pro Met  
 50 55 60

Ala Asn Lys Asn Gln Glu Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr  
 65 70 75 80

Leu Val Leu Gly Pro Leu Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn  
 85 90 95

Leu Val Ser Gln Asn Gly Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu  
 100 105 110

Glu Leu Ser Asn Glu Lys Leu Leu Asn Glu Val Lys Val Lys Asp Thr  
 115 120 125

Ala Ile Lys Asp Thr Ile Ile Glu Ile Leu Ser Ser Lys Ser Val Glu  
 130 135 140

Glu Val Val Thr Asn Lys Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys  
 145 150 155 160

Ser His Leu Asn Ser Phe Leu Ile Asp Gly Phe Ile Lys Asn Val Phe  
 165 170 175

Phe Thr Asp Phe Ile Ile Gln \*  
 180

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS042

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D

(A) NAME/KEY: CDS  
(B) POSITION: 1..858

AAA Lys	GAG Glu	TTT Phe	AAG Lys	ATT Ile	CTA Leu	ATC Ile	CTC Leu	ATT Ile	GTG Val	GTG Val	GTA Val	GTC Gly	GGC Val		48
				190				195					200		
TAT Tyr	TAT Tyr	GGG Gly	GTT Val	GAG Glu	CCT Pro	TAT Tyr	GCG Ala	CAT His	TCG Ser	GTG Val	ATG Met	CAC His	CCT Pro	AAA Lys	96
			205					210					215		
GCT Ala	CCG Pro	GCA Ala	GAT Asp	TTT Phe	GCT Ala	TTC Phe	AAG Lys	GAT Asp	TTA Leu	GAG Glu	CCG Pro	ATG Met	GAT Asp	TTA Leu	144
		220					225					230			
AAT Asn	GGC Gly	GAT Asp	GCT Ala	AAT Asn	AAG Lys	GGC Gly	AAA Lys	CAG Gln	CTT Leu	GTA Val	GCT Ala	GAA Glu	AAT Asn	TGC Cys	192
		235				240					245				
GCT Ala	TGC Cys	CAT His	GGC Gly	ATT Ile	AAA Lys	TCC Ser	CAA Gln	AAC Asn	ATT Ile	CCA Pro	GCC Ala	CCT Pro	ATG Met	GAC Asp	240
250					255					260					
CTT Leu	AGC Ser	GCG Ala	AGC Ser	AAC Asn	TCT Ser	TTT Phe	GGG Gly	GTC Val	GTG Val	CCA Pro	CCG Pro	GAT Asp	TTA Leu	AGC Ser	288
				270				275					280		
GTG Val	GCG Ala	GGG Gly	GTT Val	TTG Leu	AAC Asn	GCG Ala	AAT Asn	TTC Phe	TTA Leu	GCC Ala	CAC His	TTC Phe	ATC Ile	AAA Lys	336
			285					290					295		
CCT Pro	GTA Val	AAA Lys	ACG Thr	GCG Ala	AAA Lys	TTG Leu	AGC Ser	CAT His	AAG Lys	TTC Phe	AAC Asn	GAT Asp	GAA Glu	AGG Arg	384
		300					305					310			
TAT Tyr	CCT Pro	ATG Met	CCG Pro	GCG Ala	TTT Phe	TCT Ser	CAA Gln	TTT Phe	AGC Ser	GAT Asp	AAA Lys	GAC Asp	TTG Leu	AGC Ser	432
		315				320					325				
ATT Ile	GTG Val	GCG Ala	TAT Tyr	CTC Leu	ACT Thr	TCT Ser	ATT Ile	TTG Leu	CCT Pro	AAA Lys	AAT Asn	TTG Leu	AGC Ser	GAT Asp	480
330					335				340						
GAA Glu	GTG Val	TTC Phe	GCG Ala	CAA Gln	AGC Ser	TGT Cys	CAA Gln	AGG Arg	TGC Cys	CAT His	AGC Ser	TTG Leu	GAT Asp	TAT Tyr	528
				350				355					360		
AAA Lys	GAT Asp	AAG Lys	GCC Ala	TTT Phe	AGC Ser	GAT Asp	CCT Pro	AAA Lys	GAT Asp	CTA Leu	GCC Ala	AAT Asn	TAT Tyr	TTA Leu	576
			365				370					375			
TCT Ser	CAT His	GCA Ala	CCT Pro	GAT Asp	TTG Leu	TCC Ser	ATG Met	ATG Met	ATT Ile	AGA Arg	GCT Ala	AAA Lys	GGC Gly	GAA Glu	624
		380					385					390			

CAT GGT TTG AAT ATT TTC ATC AAC GAT CCG CAA AAG CTT TTG CCT GGC	672
His Gly Leu Asn Ile Phe Ile Asn Asp Pro Gln Lys Leu Leu Pro Gly	
395 400 405	
ACG GCT ATG CCC AGA GTG GGA TTG AGT GAA CAA GCT CAA AAA CAA GTC	720
Thr Ala Met Pro Arg Val Gly Leu Ser Glu Gln Ala Gln Lys Gln Val	
410 415 420	
ATC GCA TAT TTG GAA AAA GCA GGC GAT AGG AAA AAA CAT GAA AGG AAT	768
Ile Ala Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His Glu Arg Asn	
425 430 435 440	
ACC TTA GGG ATA AAA ATC ATG ATT TTC TTT GCG GTG CTG TCG TTC TTG	816
Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu Ser Phe Leu	
445 450 455	
GCT TAT GCG TGG AAA AGA AAA GTT TGG AGC GAA GTG CAT TGA	858
Ala Tyr Ala Trp Lys Arg Lys Val Trp Ser Glu Val His *	
460 465 470	

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Lys Glu Phe Lys Ile Leu Ile Ile Leu Ile Val Val Val Gly Val	
1 5 10 15	
Ile Tyr Tyr Gly Val Glu Pro Tyr Ala His Ser Val Met His Pro Lys	
20 25 30	
Val Ala Pro Ala Asp Phe Ala Phe Lys Asp Leu Glu Pro Met Asp Leu	
35 40 45	
Lys Asn Gly Asp Ala Asn Lys Gly Lys Gln Leu Val Ala Glu Asn Cys	
50 55 60	
Thr Ala Cys His Gly Ile Lys Ser Gln Asn Ile Pro Ala Pro Met Asp	
65 70 75 80	
Ser Leu Ser Ala Ser Asn Ser Phe Gly Val Val Pro Pro Asp Leu Ser	
85 90 95	
His Val Ala Gly Val Leu Asn Ala Asn Phe Leu Ala His Phe Ile Lys	
100 105 110	
Asp Pro Val Lys Thr Ala Lys Leu Ser His Lys Phe Asn Asp Glu Arg	
115 120 125	
Pro Tyr Pro Met Pro Ala Phe Ser Gln Phe Ser Asp Lys Asp Leu Ser	
130 135 140	
Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn Leu Ser Asp	

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145                      150                      155                      160

Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser Leu Asp Tyr  
                                 165                      170                      175

Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala Asn Tyr Leu  
                                 180                      185                      190

Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala Lys Gly Glu  
                                 195                      200                      205

His Gly Leu Asn Ile Phe Ile Asn Asp Pro Gln Lys Leu Leu Pro Gly  
                                 210                      215                      220

Thr Ala Met Pro Arg Val Gly Leu Ser Glu Gln Ala Gln Lys Gln Val  
225                                   230                      235                      240

Ile Ala Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His Glu Arg Asn  
                                 245                      250                      255

Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu Ser Phe Leu  
                                 260                      265                      270

Ala Tyr Ala Trp Lys Arg Lys Val Trp Ser Glu Val His \*

                                 275                      280                      285

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPC057 (HPC109, HPC138)

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..192

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG AAT ACA GAA ATT TTA ACC ATC ATG TTA GTT GTC TCA GTG CTT ATG	48
Met Asn Thr Glu Ile Leu Thr Ile Met Leu Val Val Ser Val Leu Met	
290                      295                      300	
GGA TTG GTA GGC TTA ATA GCG TTT TTG TGG GGG GTT AAA AGC GGT CAG	96
Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln	
305                      310                      315	
TTT GAC GAT GAA AAA CGC ATG CTT GAA AGC GTG TTG TAT GAC AGC GTG	144
Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ser Val	
320                      325                      330	
AGC GAT TTG AAC GAA GCG ATT TTA CAA GAA AAA CGC CAA AAG AAT TAA	192

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Ser Asp Leu Asn Glu Ala Ile Leu Gln Glu Lys Arg Gln Lys Asn \*  
 335 340 345 350

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Asn Thr Glu Ile Leu Thr Ile Met Leu Val Val Ser Val Leu Met  
 1 5 10 15  
 Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln  
 20 25 30  
 Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ser Val  
 35 40 45  
 Ser Asp Leu Asn Glu Ala Ile Leu Gln Glu Lys Arg Gln Lys Asn \*  
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS062 (HPS171)

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG CCC GAT TCT GCG AAC ATG ATC ATT TTA TTT TTC ACC TAT GAT ATT 48  
 Met Pro Asp Ser Ala Asn Met Ile Ile Leu Phe Phe Thr Tyr Asp Ile  
 65 70 75 80  
 TTA TTC GCT CTC AAT TAC ACC TTG CCC ATT TCC TTG CTT TTG GCG ATG 96  
 Leu Phe Ala Leu Asn Tyr Thr Leu Pro Ile Ser Leu Leu Leu Ala Met  
 85 90 95  
 GTT TTA TTT TAT ATC GCA TTC ATT AAA TCC AAC CAA TAC ACC GCC CTG 144  
 Val Leu Phe Tyr Ile Ala Phe Ile Lys Ser Asn Gln Tyr Thr Ala Leu  
 100 105 110

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CTC TCC ATT GGC TTT TCC AAA TGC CAG ATT TTA AGC CCT ATT TTT TTG Leu Ser Ile Gly Phe Ser Lys Cys Gln Ile Leu Ser Pro Ile Phe Leu 115 120 125	192
ATT AGT CTG TTT TTC ACG GCT ATT TAT GTG GGG TTG AAC GCG ACT CCT Ile Ser Leu Phe Phe Thr Ala Ile Tyr Val Gly Leu Asn Ala Thr Pro 130 135 140	240
TTT GTG TAT ATG GAA GAA AAA ACG CAA AAT TTA ATC TAT AAA GAC AAT Phe Val Tyr Met Glu Glu Lys Thr Gln Asn Leu Ile Tyr Lys Asp Asn 145 150 155 160	288
TCT TTG AGC GTC TCA GAG CAT TTG TTA GTG AAA TAT AAC GAT GAT TAC Ser Leu Ser Val Ser Glu His Leu Leu Val Lys Tyr Asn Asp Asp Tyr 165 170 175	336
GTG TAT TTT GAT AAG ATT AAT CCC CTA TTG CAA AAA GCC CAA AAC ATC Val Tyr Phe Asp Lys Ile Asn Pro Leu Leu Gln Lys Ala Gln Asn Ile 180 185 190	384
AAG GTT TTT CGC CTA AAA GAT AAG ACT TTA GAA TCT TAC GCT GAA GCT Lys Val Phe Arg Leu Lys Asp Lys Thr Leu Glu Ser Tyr Ala Glu Ala 195 200 205	432
AAA GAA GCT TTT TTT GAA GAC AAG TAT TGG ATT TTG CAT GAC ACT ACT Lys Glu Ala Phe Phe Glu Asp Lys Tyr Trp Ile Leu His Asp Thr Thr 210 215 220	480
ATC TAT GAG ATG CCC TTG AGT TTT GAA CTG GGT GCA AAC GCT TTA AGC Ile Tyr Glu Met Pro Leu Ser Phe Glu Leu Gly Ala Asn Ala Leu Ser 225 230 235 240	528
ACC ACG CGT TTA AAA ACC TTT AAA ACG CTC AAA AAT TTC CGC CCT AAA Thr Thr Arg Leu Lys Thr Phe Lys Thr Leu Lys Asn Phe Arg Pro Lys 245 250 255	576
GTT TTA GAC ACC ATT TAT CAA AAC AAG CCC GCG GTT TCT ATC ACA GAC Val Leu Asp Thr Ile Tyr Gln Asn Lys Pro Ala Val Ser Ile Thr Asp 260 265 270	624
GCT CTT TTA TCT TTG CAT GCT TTA GTG CGC CAA AAC GCA GAC ACG AAA Ala Leu Leu Ser Leu His Ala Leu Val Arg Gln Asn Ala Asp Thr Lys 275 280 285	672
AAA GTG CGA TCG TTT TTG TAT GTG TTT GCG ATT TTG CCC TTT TTT GTG Lys Val Arg Ser Phe Leu Tyr Val Phe Ala Ile Leu Pro Phe Phe Val 290 295 300	720
CCG TTT TTA AGC GTT TTA ATC GCT TAT TTT TCG CCC AGT CTC GCC CGC Pro Phe Leu Ser Val Leu Ile Ala Tyr Phe Ser Pro Ser Leu Ala Arg 305 310 315 320	768
TAT GAA AAC CTG GCT CTT TTA GGG CTA AAG TTT ATC ATT ATC ACG CTC Tyr Glu Asn Leu Ala Leu Leu Gly Leu Lys Phe Ile Ile Ile Thr Leu 325 330 335	816
GTT GTT TGG GGG CTA TTC TTT GCT TTA GGG AAG TTC AGC ATT TCA GGG Val Val Trp Gly Leu Phe Phe Ala Leu Gly Lys Phe Ser Ile Ser Gly 340 345 350	864

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ATA CTC ATT CCT GAA ATA GGC GTG CTA TCG CCC TTT TTT ATA TTC TTA 912  
 Ile Leu Ile Pro Glu Ile Gly Val Leu Ser Pro Phe Phe Ile Phe Leu  
 355 360 365

GCT CTT AGT CTT TGG TAT TTT AAA AAG CTT AAT AAG AGG TTG TAG 957  
 Ala Leu Ser Leu Trp Tyr Phe Lys Lys Leu Asn Lys Arg Leu \*  
 370 375 380

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Pro Asp Ser Ala Asn Met Ile Ile Leu Phe Phe Thr Tyr Asp Ile  
 1 5 10 15  
 Leu Phe Ala Leu Asn Tyr Thr Leu Pro Ile Ser Leu Leu Leu Ala Met  
 20 25 30  
 Val Leu Phe Tyr Ile Ala Phe Ile Lys Ser Asn Gln Tyr Thr Ala Leu  
 35 40 45  
 Leu Ser Ile Gly Phe Ser Lys Cys Gln Ile Leu Ser Pro Ile Phe Leu  
 50 55 60  
 Ile Ser Leu Phe Phe Thr Ala Ile Tyr Val Gly Leu Asn Ala Thr Pro  
 65 70 75 80  
 Phe Val Tyr Met Glu Glu Lys Thr Gln Asn Leu Ile Tyr Lys Asp Asn  
 85 90 95  
 Ser Leu Ser Val Ser Glu His Leu Leu Val Lys Tyr Asn Asp Asp Tyr  
 100 105 110  
 Val Tyr Phe Asp Lys Ile Asn Pro Leu Leu Gln Lys Ala Gln Asn Ile  
 115 120 125  
 Lys Val Phe Arg Leu Lys Asp Lys Thr Leu Glu Ser Tyr Ala Glu Ala  
 130 135 140  
 Lys Glu Ala Phe Phe Glu Asp Lys Tyr Trp Ile Leu His Asp Thr Thr  
 145 150 155 160  
 Ile Tyr Glu Met Pro Leu Ser Phe Glu Leu Gly Ala Asn Ala Leu Ser  
 165 170 175  
 Thr Thr Arg Leu Lys Thr Phe Lys Thr Leu Lys Asn Phe Arg Pro Lys  
 180 185 190  
 Val Leu Asp Thr Ile Tyr Gln Asn Lys Pro Ala Val Ser Ile Thr Asp  
 195 200 205

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Ala Leu Leu Ser Leu His Ala Leu Val Arg Gln Asn Ala Asp Thr Lys  
 210 215 220

Lys Val Arg Ser Phe Leu Tyr Val Phe Ala Ile Leu Pro Phe Phe Val  
 225 230 235 240

Pro Phe Leu Ser Val Leu Ile Ala Tyr Phe Ser Pro Ser Leu Ala Arg  
 245 250 255

Tyr Glu Asn Leu Ala Leu Leu Gly Leu Lys Phe Ile Ile Ile Thr Leu  
 260 265 270

Val Val Trp Gly Leu Phe Phe Ala Leu Gly Lys Phe Ser Ile Ser Gly  
 275 280 285

Ile Leu Ile Pro Glu Ile Gly Val Leu Ser Pro Phe Phe Ile Phe Leu  
 290 295 300

Ala Leu Ser Leu Trp Tyr Phe Lys Lys Leu Asn Lys Arg Leu \*

305

310

315

## (2) INFORMATION FOR SEQ ID NO: 15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1629 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS065 (HPS153)

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..1629

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATG AAT AAA CCA TTT TTA ATC TTA CTC ATA GCC CTA ATT GTC TTT AGC	48
Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Val Phe Ser	
320 325 330 335	
GGC TGT AAC ATG AGA AAA TAT TTC AAA CCC GCT AAA CAC CAA ATT AAA	96
Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys	
340 345 350	
GGC GAA GCG TAT TTC CCT AAC CAT TTG CAA GAA AGT ATC GTT TCG TCT	144
Gly Glu Ala Tyr Phe Pro Asn His Leu Gln Glu Ser Ile Val Ser Ser	
355 360 365	
AAT CGT TAT GGA GCC ATT TTG AAA AAT GGA GCG GTT ATA GGC GAT AAA	192
Asn Arg Tyr Gly Ala Ile Leu Lys Asn Gly Ala Val Ile Gly Asp Lys	
370 375 380	
GGT TTA ACG CAG CTA AGA ATC GGT AAG AAC TTC AAT TAC GAA AGC AGT	240
Gly Leu Thr Gln Leu Arg Ile Gly Lys Asn Phe Asn Tyr Glu Ser Ser	

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385	390	395	
TTT TTA AAT GAG AGT CAA GGG TTT TTT ATT CTT GCG CAA GAT TGT TTG Phe Leu Asn Glu Ser Gln Gly Phe Phe Ile Leu Ala Gln Asp Cys Leu 400 405 410 415			288
AAC AAG ATT GAT AAA AAA ACA AAC AAA AGC AAG GTG GCT AAG ACT GAA Asn Lys Ile Asp Lys Lys Thr Asn Lys Ser Lys Val Ala Lys Thr Glu 420 425 430			336
GAA ACG GAA TTG AAA TTA AAG GGC GTT GAA GCG GAA GTC CAA GAT AAA Glu Thr Glu Leu Lys Leu Lys Gly Val Glu Ala Glu Val Gln Asp Lys 435 440 445			384
GTC TGT CAT CAA GTG GAA TTG ATT AGC AAT AAC CCT AAC GCC AGC CAA Val Cys His Gln Val Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln 450 455 460			432
CAA TCT ATC GTT ATT CCT TTG GAG ACT TTT GCC TTG AGC GCA AGC GTT Gln Ser Ile Val Ile Pro Leu Glu Thr Phe Ala Leu Ser Ala Ser Val 465 470 475			480
AAA GGG AAT CTT TTA GCG GTG GTG TTA GCG GAC AAT TCA GCG AAC TTA Lys Gly Asn Leu Leu Ala Val Val Leu Ala Asp Asn Ser Ala Asn Leu 480 485 490 495			528
TAC GAC ATC ACT TCT CAA AAA TTG CTT TTT AGT GAG AAA GGT TCC CCA Tyr Asp Ile Thr Ser Gln Lys Leu Leu Phe Ser Glu Lys Gly Ser Pro 500 505 510			576
AGC ACC ACG ATC AAT TCT TTA ATG GCG ATG CCT ATT TTT ATG GAT ACG Ser Thr Thr Ile Asn Ser Leu Met Ala Met Pro Ile Phe Met Asp Thr 515 520 525			624
GTC GTG GTG TTC CCC ATG CTA GAT GGG CGC TTG TTG GTC GTG GAT TAT Val Val Val Phe Pro Met Leu Asp Gly Arg Leu Leu Val Val Asp Tyr 530 535 540			672
GTG CAC GGA AAC CCT ACG CCT ATT AGA AAC ATT GTT ATC AGC AGC GAT Val His Gly Asn Pro Thr Pro Ile Arg Asn Ile Val Ile Ser Ser Asp 545 550 555			720
AAG TTT TTT AAC AAT ATC ACC TAC CTT ATC GTA GAT GGC AAT AAC ATG Lys Phe Phe Asn Asn Ile Thr Tyr Leu Ile Val Asp Gly Asn Asn Met 560 565 570 575			768
ATC GCT TCT ACA GGG AAA AGG ATA CTC TCA GTA GTG AGC GGT CAA GAG Ile Ala Ser Thr Gly Lys Arg Ile Leu Ser Val Val Ser Gly Gln Glu 580 585 590			816
TTC AAC TAT GAT GGG GAT ATT GTG GAT TTG CTT TAT GAT AAG GGG ACT Phe Asn Tyr Asp Gly Asp Ile Val Asp Leu Leu Tyr Asp Lys Gly Thr 595 600 605			864
TTA TAT GTG CTC ACG CTA GAC GGG CAG ATT TTG CAA ATG GAT AAG AGT Leu Tyr Val Leu Thr Leu Asp Gly Gln Ile Leu Gln Met Asp Lys Ser 610 615 620			912
TTG AGG GAA TTA AAC AGC GTG AAA CTG CCT TCG TCG CTC AAC ACG ATT			960

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Leu	Arg	Glu	Leu	Asn	Ser	Val	Lys	Leu	Pro	Ser	Ser	Leu	Asn	Thr	Ile	
625						630					635					
GTA	TTA	AAC	CAT	AAT	AAA	TTG	TAT	TCT	TTA	GAA	AAA	CGA	GGG	TAT	GTG	1008
Val	Leu	Asn	His	Asn	Lys	Leu	Tyr	Ser	Leu	Glu	Lys	Arg	Gly	Tyr	Val	
640					645					650					655	
ATA	GAG	GTG	GAT	TTA	AAT	GAT	TTT	GAT	TCG	TAT	AAT	GTC	TAT	AAA	ACG	1056
Ile	Glu	Val	Asp	Leu	Asn	Asp	Phe	Asp	Ser	Tyr	Asn	Val	Tyr	Lys	Thr	
				660					665					670		
CCA	ACT	ATA	GGC	AGT	TTT	AAG	TTT	TTT	TCA	TCT	AAT	CGT	TTG	GAT	AAA	1104
Pro	Thr	Ile	Gly	Ser	Phe	Lys	Phe	Phe	Ser	Ser	Asn	Arg	Leu	Asp	Lys	
			675					680					685			
GGG	GTG	TTT	TAT	GAT	AAA	AAT	CGG	GTG	TAT	TAC	GAT	CGC	TAC	TAT	TTA	1152
Gly	Val	Phe	Tyr	Asp	Lys	Asn	Arg	Val	Tyr	Tyr	Asp	Arg	Tyr	Tyr	Leu	
		690					695					700				
GAT	TAT	AAC	GAT	TTT	AAA	CCA	AAA	CTT	TAT	CCC	GTT	GTG	GAA	AAA	TCG	1200
Asp	Tyr	Asn	Asp	Phe	Lys	Pro	Lys	Leu	Tyr	Pro	Val	Val	Glu	Lys	Ser	
	705					710					715					
GCA	TCT	AAA	AAA	TCT	CAA	AAA	GGC	GAA	AAA	GGG	AAC	GCT	CCT	ATT	TAT	1248
Ala	Ser	Lys	Lys	Ser	Gln	Lys	Gly	Glu	Lys	Gly	Asn	Ala	Pro	Ile	Tyr	
720					725					730					735	
TTG	CAA	GAA	AGG	CAT	AAA	GCT	AAA	GAA	AAT	AAA	CAG	CCT	TTA	GAA	GAA	1296
Leu	Gln	Glu	Arg	His	Lys	Ala	Lys	Glu	Asn	Lys	Gln	Pro	Leu	Glu	Glu	
				740					745					750		
AAC	AAA	GTT	AAA	CCA	AGA	AAT	AGC	GGG	TTT	GAA	GAA	GAA	GAG	GTT	AAA	1344
Asn	Lys	Val	Lys	Pro	Arg	Asn	Ser	Gly	Phe	Glu	Glu	Glu	Glu	Val	Lys	
			755					760					765			
ACC	AGA	AGG	CCT	GAG	CCT	ATT	AGG	GAT	CAA	AAT	AAC	GCC	ACC	CAA	CAA	1392
Thr	Arg	Arg	Pro	Glu	Pro	Ile	Arg	Asp	Gln	Asn	Asn	Ala	Thr	Gln	Gln	
			770				775					780				
GGC	GAA	ACA	AAA	AAC	AAT	GAA	AGT	AAA	AAC	GCT	CCT	GTC	TTA	AAA	GAA	1440
Gly	Glu	Thr	Lys	Asn	Asn	Glu	Ser	Lys	Asn	Ala	Pro	Val	Leu	Lys	Glu	
	785					790				795						
AAC	GCC	GCT	AAA	AAA	GAA	GTG	CCA	AAA	CCA	AAT	TCT	AAA	GAA	GAA	AAA	1488
Asn	Ala	Ala	Lys	Lys	Glu	Val	Pro	Lys	Pro	Asn	Ser	Lys	Glu	Glu	Lys	
800					805					810					815	
CGC	CGC	TTG	AAA	GAA	GAA	AAG	AAA	AAA	GCC	AAA	GCC	GAA	CAA	AGA	GCG	1536
Arg	Arg	Leu	Lys	Glu	Glu	Lys	Lys	Lys	Ala	Lys	Ala	Glu	Gln	Arg	Ala	
				820					825					830		
AGA	GAA	TTT	GAA	CAA	AGA	GCG	AGA	GAG	CAT	CAA	GAA	AGA	GAT	GAA	AAA	1584
Arg	Glu	Phe	Glu	Gln	Arg	Ala	Arg	Glu	His	Gln	Glu	Arg	Asp	Glu	Lys	
			835					840					845			
GAG	CTT	GAA	GAA	AGA	AGA	AAA	GCT	TTA	GAA	ATG	AAT	AAG	AAG	TAG		1629
Glu	Leu	Glu	Glu	Arg	Arg	Lys	Ala	Leu	Glu	Met	Asn	Lys	Lys	*		
	850						855					860				

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## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 Amino acids

(B) TYPE: Amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Val Phe Ser  
 1 5 10 15

Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys  
 20 25 30

Gly Glu Ala Tyr Phe Pro Asn His Leu Gln Glu Ser Ile Val Ser Ser  
 35 40 45

Asn Arg Tyr Gly Ala Ile Leu Lys Asn Gly Ala Val Ile Gly Asp Lys  
 50 55 60

Gly Leu Thr Gln Leu Arg Ile Gly Lys Asn Phe Asn Tyr Glu Ser Ser  
 65 70 75 80

Phe Leu Asn Glu Ser Gln Gly Phe Phe Ile Leu Ala Gln Asp Cys Leu  
 85 90 95

Asn Lys Ile Asp Lys Lys Thr Asn Lys Ser Lys Val Ala Lys Thr Glu  
 100 105 110

Glu Thr Glu Leu Lys Leu Lys Gly Val Glu Ala Glu Val Gln Asp Lys  
 115 120 125

Val Cys His Gln Val Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln  
 130 135 140

Gln Ser Ile Val Ile Pro Leu Glu Thr Phe Ala Leu Ser Ala Ser Val  
 145 150 155 160

Lys Gly Asn Leu Leu Ala Val Val Leu Ala Asp Asn Ser Ala Asn Leu  
 165 170 175

Tyr Asp Ile Thr Ser Gln Lys Leu Leu Phe Ser Glu Lys Gly Ser Pro  
 180 185 190

Ser Thr Thr Ile Asn Ser Leu Met Ala Met Pro Ile Phe Met Asp Thr  
 195 200 205

Val Val Val Phe Pro Met Leu Asp Gly Arg Leu Leu Val Val Asp Tyr  
 210 215 220

Val His Gly Asn Pro Thr Pro Ile Arg Asn Ile Val Ile Ser Ser Asp  
 225 230 235 240

Lys Phe Phe Asn Asn Ile Thr Tyr Leu Ile Val Asp Gly Asn Asn Met  
 245 250 255

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Ile Ala Ser Thr Gly Lys Arg Ile Leu Ser Val Val Ser Gly Gln Glu  
 260 265 270  
 Phe Asn Tyr Asp Gly Asp Ile Val Asp Leu Leu Tyr Asp Lys Gly Thr  
 275 280 285  
 Leu Tyr Val Leu Thr Leu Asp Gly Gln Ile Leu Gln Met Asp Lys Ser  
 290 295 300  
 Leu Arg Glu Leu Asn Ser Val Lys Leu Pro Ser Ser Leu Asn Thr Ile  
 305 310 315 320  
 Val Leu Asn His Asn Lys Leu Tyr Ser Leu Glu Lys Arg Gly Tyr Val  
 325 330 335  
 Ile Glu Val Asp Leu Asn Asp Phe Asp Ser Tyr Asn Val Tyr Lys Thr  
 340 345 350  
 Pro Thr Ile Gly Ser Phe Lys Phe Phe Ser Ser Asn Arg Leu Asp Lys  
 355 360 365  
 Gly Val Phe Tyr Asp Lys Asn Arg Val Tyr Tyr Asp Arg Tyr Tyr Leu  
 370 375 380  
 Asp Tyr Asn Asp Phe Lys Pro Lys Leu Tyr Pro Val Val Glu Lys Ser  
 385 390 395 400  
 Ala Ser Lys Lys Ser Gln Lys Gly Glu Lys Gly Asn Ala Pro Ile Tyr  
 405 410 415  
 Leu Gln Glu Arg His Lys Ala Lys Glu Asn Lys Gln Pro Leu Glu Glu  
 420 425 430  
 Asn Lys Val Lys Pro Arg Asn Ser Gly Phe Glu Glu Glu Glu Val Lys  
 435 440 445  
 Thr Arg Arg Pro Glu Pro Ile Arg Asp Gln Asn Asn Ala Thr Gln Gln  
 450 455 460  
 Gly Glu Thr Lys Asn Asn Glu Ser Lys Asn Ala Pro Val Leu Lys Glu  
 465 470 475 480  
 Asn Ala Ala Lys Lys Glu Val Pro Lys Pro Asn Ser Lys Glu Glu Lys  
 485 490 495  
 Arg Arg Leu Lys Glu Glu Lys Lys Lys Ala Lys Ala Glu Gln Arg Ala  
 500 505 510  
 Arg Glu Phe Glu Gln Arg Ala Arg Glu His Gln Glu Arg Asp Glu Lys  
 515 520 525  
 Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu Met Asn Lys Lys \*  
 530 535 540

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 Base pairs

(B) TYPE: Nucleotide

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(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS066

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) POSITION:1..1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATG CTT GAA ACT TCT AGC CAT TTT TTA AAA TCG TTT CGC TTG AAG CGT	48
Met Leu Glu Thr Ser Ser His Phe Leu Lys Ser Phe Arg Leu Lys Arg	
545 550 555	
TAT ATA GGG TTT TTA TTG ATT TCT TTA GCG TTA TTA ATC ACG CCC TTT	96
Tyr Ile Gly Phe Leu Leu Ile Ser Leu Ala Leu Leu Ile Thr Pro Phe	
560 565 570 575	
GTT CGC ATT GAT GGG GCG CAT TTG TTT TTG ATC TCT TTT GAG CAT AAG	144
Val Arg Ile Asp Gly Ala His Leu Phe Leu Ile Ser Phe Glu His Lys	
580 585 590	
CAA CTG CAT TTT TTA GGC AAG ATC TTT AGC GCT GAA GAA TTG CAA GTC	192
Gln Leu His Phe Leu Gly Lys Ile Phe Ser Ala Glu Glu Leu Gln Val	
595 600 605	
ATG CCT TTT ATG GTT ATT TTG CTT TTT ATA GGG ATT TTT TTC ATC ACC	240
Met Pro Phe Met Val Ile Leu Leu Phe Ile Gly Ile Phe Phe Ile Thr	
610 615 620	
ACT AGC CTT GGG CGT GTG TGG TGC GGT TGG GCT TGC CCG CAA ACC TTT	288
Thr Ser Leu Gly Arg Val Trp Cys Gly Trp Ala Cys Pro Gln Thr Phe	
625 630 635	
TTA AGG GTG CTT TAT AGA GAT GTG ATT GAA ACC AAG ATT TTC AAA CTC	336
Leu Arg Val Leu Tyr Arg Asp Val Ile Glu Thr Lys Ile Phe Lys Leu	
640 645 650 655	
CAT AAA AAG ATC AGC AAC AAG CAA GAA AGC CCT AAA AAC ACC CCA AGC	384
His Lys Lys Ile Ser Asn Lys Gln Glu Ser Pro Lys Asn Thr Pro Ser	
660 665 670	
TAC AAG ATC CGT AAA GTA TTG AGC GTT TTA TTG TTC GCT CCT GTT GTG	432
Tyr Lys Ile Arg Lys Val Leu Ser Val Leu Leu Phe Ala Pro Val Val	
675 680 685	
GCG GGG CTA ATG ATG TTG TTT TTC TTT TAT TTC ATC GCC CCA GAA GAT	480
Ala Gly Leu Met Met Leu Phe Phe Phe Tyr Phe Ile Ala Pro Glu Asp	
690 695 700	
TTT TTT ATG TAT CTT AAA AAC CCT AGC GAT CAC CCT ATT GCT ATG GGT	528
Phe Phe Met Tyr Leu Lys Asn Pro Ser Asp His Pro Ile Ala Met Gly	
705 710 715	

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TTT TGG CTT TTT AGC ACG GCT GTG GTG CTA TTT GAT ATA GTG GTG GTT Phe Trp Leu Phe Ser Thr Ala Val Val Leu Phe Asp Ile Val Val Val 720 725 730 735	576
GCG GAG CGT TTT TGC ATT TAT TTA TGC CCT TAC GCT AGG GTG CAA TCG Ala Glu Arg Phe Cys Ile Tyr Leu Cys Pro Tyr Ala Arg Val Gln Ser 740 745 750	624
GTG TTG TAT GAC AAT GAC ACC TTA AAC CCT ATT TAT GAT GAA AAG CGC Val Leu Tyr Asp Asn Asp Thr Leu Asn Pro Ile Tyr Asp Glu Lys Arg 755 760 765	672
GGC GGA GCG CTT TAT AAT AAT CAG GGC CAT CTC TTC CCC TTA CCT CCC Gly Gly Ala Leu Tyr Asn Asn Gln Gly His Leu Phe Pro Leu Pro Pro 770 775 780	720
AAA AAA CGC AGC CCA GAA AAC GAA TGC GTG AAT TGT TTG CAT TGC GTG Lys Lys Arg Ser Pro Glu Asn Glu Cys Val Asn Cys Leu His Cys Val 785 790 795	768
CAG GTT TGC CCC ACG CAT ATT GAC ATC AGG AAG GGC TTG CAA TTA GAA Gln Val Cys Pro Thr His Ile Asp Ile Arg Lys Gly Leu Gln Leu Glu 800 805 810 815	816
TGC ATC AAT TGT TTA GAA TGC GTG GAT GCA TGC ACG ATT ACC ATG GCT Cys Ile Asn Cys Leu Glu Cys Val Asp Ala Cys Thr Ile Thr Met Ala 820 825 830	864
AAA TTT AAC CGC CCT TCA CTC ATC CAA TGG TCT TCA ACT AAC GCT ATT Lys Phe Asn Arg Pro Ser Leu Ile Gln Trp Ser Ser Thr Asn Ala Ile 835 840 845	912
AAT ACG CGC CAA AAA GTG CAC CTG GTG CGT TTA AAA ACG ATC GCT TAC Asn Thr Arg Gln Lys Val His Leu Val Arg Leu Lys Thr Ile Ala Tyr 850 855 860	960
ATG GGG GTT ATC GCT ATT GTG ATC GCT CTT TTA GCC ATC ACT TCG TTT Met Gly Val Ile Ala Ile Val Ile Ala Leu Leu Ala Ile Thr Ser Phe 865 870 875	1008
AAA AAA GAA CGC ATG CTC TTA GAC ATT AAC CGC AAC AGC GAT CTG TAT Lys Lys Glu Arg Met Leu Leu Asp Ile Asn Arg Asn Ser Asp Leu Tyr 880 885 890 895	1056
GAA TTG CGC TCT AGC GGG TAT GTG GAT AAC GAT TAC GTG TTT TTA TTC Glu Leu Arg Ser Ser Gly Tyr Val Asp Asn Asp Tyr Val Phe Leu Phe 900 905 910	1104
CAC AAC ACG GAC AAT AAA GAC CAT GAG TTT TAT TTC AAA GTT TTA GGG His Asn Thr Asp Asn Lys Asp His Glu Phe Tyr Phe Lys Val Leu Gly 915 920 925	1152
CAA AAA GAC ATT CAG ATC AAA AAG CCT TTA AAT CCT ATC GCC ATT AAA Gln Lys Asp Ile Gln Ile Lys Lys Pro Leu Asn Pro Ile Ala Ile Lys 930 935 940	1200
GCC GGG CAA AAG ATT AAA GCG GTA GTG ATT TTA AGA AAA CCC CTA AAG Ala Gly Gln Lys Ile Lys Ala Val Val Ile Leu Arg Lys Pro Leu Lys 945 950 955	1248

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AGT AAC GCC ACA GAA TAC AAG AAC GCT AAA GAC GCT CTA ATC CCC ATT 1296  
 Ser Asn Ala Thr Glu Tyr Lys Asn Ala Lys Asp Ala Leu Ile Pro Ile  
 960 965 970 975

ACC ATA CAA GCT TAT AGC GCG GAC GAT AAG AAT ATT ACG ATA GAA AGG 1344  
 Thr Ile Gln Ala Tyr Ser Ala Asp Asp Lys Asn Ile Thr Ile Glu Arg  
 980 985 990

GAA TCG GTG TTT ATT GCA CCA AGT GAG GAT TGA 1377  
 Glu Ser Val Phe Ile Ala Pro Ser Glu Asp \*  
 995 1000

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Leu Glu Thr Ser Ser His Phe Leu Lys Ser Phe Arg Leu Lys Arg  
 1 5 10 15  
 Tyr Ile Gly Phe Leu Leu Ile Ser Leu Ala Leu Leu Ile Thr Pro Phe  
 20 25 30  
 Val Arg Ile Asp Gly Ala His Leu Phe Leu Ile Ser Phe Glu His Lys  
 35 40 45  
 Gln Leu His Phe Leu Gly Lys Ile Phe Ser Ala Glu Glu Leu Gln Val  
 50 55 60  
 Met Pro Phe Met Val Ile Leu Leu Phe Ile Gly Ile Phe Phe Ile Thr  
 65 70 75 80  
 Thr Ser Leu Gly Arg Val Trp Cys Gly Trp Ala Cys Pro Gln Thr Phe  
 85 90 95  
 Leu Arg Val Leu Tyr Arg Asp Val Ile Glu Thr Lys Ile Phe Lys Leu  
 100 105 110  
 His Lys Lys Ile Ser Asn Lys Gln Glu Ser Pro Lys Asn Thr Pro Ser  
 115 120 125  
 Tyr Lys Ile Arg Lys Val Leu Ser Val Leu Leu Phe Ala Pro Val Val  
 130 135 140  
 Ala Gly Leu Met Met Leu Phe Phe Phe Tyr Phe Ile Ala Pro Glu Asp  
 145 150 155 160  
 Phe Phe Met Tyr Leu Lys Asn Pro Ser Asp His Pro Ile Ala Met Gly  
 165 170 175  
 Phe Trp Leu Phe Ser Thr Ala Val Val Leu Phe Asp Ile Val Val Val  
 180 185 190

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Ala Glu Arg Phe Cys Ile Tyr Leu Cys Pro Tyr Ala Arg Val Gln Ser  
195 200 205

Val Leu Tyr Asp Asn Asp Thr Leu Asn Pro Ile Tyr Asp Glu Lys Arg  
210 215 220

Gly Gly Ala Leu Tyr Asn Asn Gln Gly His Leu Phe Pro Leu Pro Pro  
225 230 235 240

Lys Lys Arg Ser Pro Glu Asn Glu Cys Val Asn Cys Leu His Cys Val  
245 250 255

Gln Val Cys Pro Thr His Ile Asp Ile Arg Lys Gly Leu Gln Leu Glu  
260 265 270

Cys Ile Asn Cys Leu Glu Cys Val Asp Ala Cys Thr Ile Thr Met Ala  
275 280 285

Lys Phe Asn Arg Pro Ser Leu Ile Gln Trp Ser Ser Thr Asn Ala Ile  
290 295 300

Asn Thr Arg Gln Lys Val His Leu Val Arg Leu Lys Thr Ile Ala Tyr  
305 310 315 320

Met Gly Val Ile Ala Ile Val Ile Ala Leu Leu Ala Ile Thr Ser Phe  
325 330 335

Lys Lys Glu Arg Met Leu Leu Asp Ile Asn Arg Asn Ser Asp Leu Tyr  
340 345 350

Glu Leu Arg Ser Ser Gly Tyr Val Asp Asn Asp Tyr Val Phe Leu Phe  
355 360 365

His Asn Thr Asp Asn Lys Asp His Glu Phe Tyr Phe Lys Val Leu Gly  
370 375 380

Gln Lys Asp Ile Gln Ile Lys Lys Pro Leu Asn Pro Ile Ala Ile Lys  
385 390 395 400

Ala Gly Gln Lys Ile Lys Ala Val Val Ile Leu Arg Lys Pro Leu Lys  
405 410 415

Ser Asn Ala Thr Glu Tyr Lys Asn Ala Lys Asp Ala Leu Ile Pro Ile  
420 425 430

Thr Ile Gln Ala Tyr Ser Ala Asp Asp Lys Asn Ile Thr Ile Glu Arg  
435 440 445

Glu Ser Val Phe Ile Ala Pro Ser Glu Asp \*

450 455

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1533 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

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(vii) DIRECT SOURCE:

(B) CLONE(S): HPS068

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) POSITION:1..1533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG AAA AAA ACA ACC CTC TTT GTA TTG GGC TTA TTA TTT AAT AGC TTT	48
Met Lys Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser Phe	
460 465 470 475	
TTA AAT GCT GTT GAT GGG ATT TCT AAA ACC GAT CTT TCT TCT TTG AAT	96
Leu Asn Ala Val Asp Gly Ile Ser Lys Thr Asp Leu Ser Ser Leu Asn	
480 485 490	
TTG GCT GAA GAC AGC GCG CCT TTG AAC CAT CCT AAC GCT CAA AAA CTC	144
Leu Ala Glu Asp Ser Ala Pro Leu Asn His Pro Asn Ala Gln Lys Leu	
495 500 505	
TCC TTA AAA AAC GCA TGG ACT AGG GTA TTG TCT AAC CAT GAA GGC TTG	192
Ser Leu Lys Asn Ala Trp Thr Arg Val Leu Ser Asn His Glu Gly Leu	
510 515 520	
CAT GCG CAA GAA TAC GCC ATT AAG CGA GCG AGT AAA ATG AAA TTA GCG	240
His Ala Gln Glu Tyr Ala Ile Lys Arg Ala Ser Lys Met Lys Leu Ala	
525 530 535	
GCT AAA CTT TCT TTT TTG CCT CAA ATT GAT TTG AGC GCT TTT TAT GTG	288
Ala Lys Leu Ser Phe Leu Pro Gln Ile Asp Leu Ser Ala Phe Tyr Val	
540 545 550 555	
TAT CTC TCT AAC CCC ATT AAA ATG GAT TTT GCC AGC CAA AAA CAA CCG	336
Tyr Leu Ser Asn Pro Ile Lys Met Asp Phe Ala Ser Gln Lys Gln Pro	
560 565 570	
GGC GTG CAA AAA GCC ACC AAC CAG ATC CAT CAA GGC ATA CAA AAC ATC	384
Gly Val Gln Lys Ala Thr Asn Gln Ile His Gln Gly Ile Gln Asn Ile	
575 580 585	
CAG CAA AAT ATC CCT TCT CAA GTA TTA ACC CCT CAA ATC CAA GCG GGC	432
Gln Gln Asn Ile Pro Ser Gln Val Leu Thr Pro Gln Ile Gln Ala Gly	
590 595 600	
ATG CAA GGG GTG ATG CAA GGT TTT GGG GCT TTG AGC AGC ACT TTA GAA	480
Met Gln Gly Val Met Gln Gly Phe Gly Ala Leu Ser Ser Thr Leu Glu	
605 610 615	
GCC CCC TTA TTG TTT TCT AAG CAA AAT GTG GTG ATT GGG GCT TTG AGC	528
Ala Pro Leu Leu Phe Ser Lys Gln Asn Val Val Ile Gly Ala Leu Ser	
620 625 630 635	
ATT ATT TAT CCC CTT TAT ATG GGT GGG GCA AGA TTC ACG ATG GTG CGC	576
Ile Ile Tyr Pro Leu Tyr Met Gly Gly Ala Arg Phe Thr Met Val Arg	

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640	645	650	
ATT GCG GAT TTG ATG CAA AAA GAT GCT AAT GAA GTG TAT CGT TTG AAA Ile Ala Asp Leu Met Gln Lys Asp Ala Asn Glu Val Tyr Arg Leu Lys 655 660 665			624
AAG CTT TCC ACT TTT CAA GAG CTT GTG AGC GTG TAT TAC GGC ATG GTG Lys Leu Ser Thr Phe Gln Glu Leu Val Ser Val Tyr Tyr Gly Met Val 670 675 680			672
TTA AAC GCA GAA GTG GCT GAA ACT TTA GAA GAG GTG GAA AAA GGC CAT Leu Asn Ala Glu Val Ala Glu Thr Leu Glu Glu Val Glu Lys Gly His 685 690 695			720
TAT AAG CAT TTC CAA AAC GCT TTG AAA ATG CAA AAA GTG GGG CAA ATC Tyr Lys His Phe Gln Asn Ala Leu Lys Met Gln Lys Val Gly Gln Ile 700 705 710 715			768
GCT AGG GTA GAA ACC TTA GGC GCT CAA GTG GCT TAT GAT AAG GCC CAT Ala Arg Val Glu Thr Leu Gly Ala Gln Val Ala Tyr Asp Lys Ala His 720 725 730			816
ATC GCT AGC GTT AAG GCT AAA GAC GTG TTA GAA GTT TCG CAG CTC TCG Ile Ala Ser Val Lys Ala Lys Asp Val Leu Glu Val Ser Gln Leu Ser 735 740 745			864
TTC AAT TCC ATT TTA TCT AGC AAG GAC GAT TTA GTG CCT TCA AGC AAA Phe Asn Ser Ile Leu Ser Ser Lys Asp Asp Leu Val Pro Ser Ser Lys 750 755 760			912
TTA GAG ATC CGC ACG GAG AAA AAT CTG CCC GAT CTG AGC TTT TTT GTT Leu Glu Ile Arg Thr Glu Lys Asn Leu Pro Asp Leu Ser Phe Phe Val 765 770 775			960
TCT TCC ACG CTC AAT TCC TAC CCG GTT TTA AAG ACT TTA GAA AAT CAG Ser Ser Thr Leu Asn Ser Tyr Pro Val Leu Lys Thr Leu Glu Asn Gln 780 785 790 795			1008
ATT CAA ATC TCT AAA GAA AAC ACG AAA TTA CAG ATC GCT AAA TTC TTG Ile Gln Ile Ser Lys Glu Asn Thr Lys Leu Gln Ile Ala Lys Phe Leu 800 805 810			1056
CCC CAA GTG AGT TTT TTT GGC TCT TAT ATT ATG AAG CAA AAC AAT TCG Pro Gln Val Ser Phe Phe Gly Ser Tyr Ile Met Lys Gln Asn Asn Ser 815 820 825			1104
GTG TTT GAA GAC ATG ATC CCT AGT TGG TTT GTG GGC GTG GCC GGG CGC Val Phe Glu Asp Met Ile Pro Ser Trp Phe Val Gly Val Ala Gly Arg 830 835 840			1152
ATG CCT ATT CTT TCT CCC ACA GGG CGC ATT CAA AAA TAC CAA GCG AGC Met Pro Ile Leu Ser Pro Thr Gly Arg Ile Gln Lys Tyr Gln Ala Ser 845 850 855			1200
AAA TTA GCG GAG TTG CAA GTG AGT AGC GAA CAA ATC CAG GCT AAA AAA Lys Leu Ala Glu Leu Gln Val Ser Ser Glu Gln Ile Gln Ala Lys Lys 860 865 870 875			1248
AAC ATG GAA TTA TTA GTG AAT AAG ACT TAT AAA GAG ACG CTT TCT TAT			1296

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Asn Met Glu Leu Leu Val Asn Lys Thr Tyr Lys Glu Thr Leu Ser Tyr  
880 885 890

TTG AAA GAA TAC AAA AGC TTG CTT TCT AGC GTG GAA TTA GCC AAG GAA 1344  
Leu Lys Glu Tyr Lys Ser Leu Leu Ser Ser Val Glu Leu Ala Lys Glu  
895 900 905

AAC TTA AAA CTC CAA GAG CAG GCT TTT TTA CAA GGC TTA AGC ACG AAC 1392  
Asn Leu Lys Leu Gln Glu Gln Ala Phe Leu Gln Gly Leu Ser Thr Asn  
910 915 920

GCT CAA GTC ATT GAT GCG AGG AAC ACG CTT TCT TCT ATC GTC GTG GAG 1440  
Ala Gln Val Ile Asp Ala Arg Asn Thr Leu Ser Ser Ile Val Val Glu  
925 930 935

CAA AAA AGC GTG GCT TAT AAA TAC ATC GTT TCA TTA GCG AAT TTA ATG 1488  
Gln Lys Ser Val Ala Tyr Lys Tyr Ile Val Ser Leu Ala Asn Leu Met  
940 945 950 955

GCG TTA AGC GAT CAT ATT GAT TTA TTT TAT GAA TTT GTT TAT TAA 1533  
Ala Leu Ser Asp His Ile Asp Leu Phe Tyr Glu Phe Val Tyr \*  
960 965 970

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 Amino acids  
(B) TYPE: Amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Lys Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser Phe  
1 5 10 15

Leu Asn Ala Val Asp Gly Ile Ser Lys Thr Asp Leu Ser Ser Leu Asn  
20 25 30

Leu Ala Glu Asp Ser Ala Pro Leu Asn His Pro Asn Ala Gln Lys Leu  
35 40 45

Ser Leu Lys Asn Ala Trp Thr Arg Val Leu Ser Asn His Glu Gly Leu  
50 55 60

His Ala Gln Glu Tyr Ala Ile Lys Arg Ala Ser Lys Met Lys Leu Ala  
65 70 75 80

Ala Lys Leu Ser Phe Leu Pro Gln Ile Asp Leu Ser Ala Phe Tyr Val  
85 90 95

Tyr Leu Ser Asn Pro Ile Lys Met Asp Phe Ala Ser Gln Lys Gln Pro  
100 105 110

Gly Val Gln Lys Ala Thr Asn Gln Ile His Gln Gly Ile Gln Asn Ile  
115 120 125

Gln Gln Asn Ile Pro Ser Gln Val Leu Thr Pro Gln Ile Gln Ala Gly

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130	135	140
Met Gln Gly Val 145	Met Gln Gly Phe Gly Ala 150	Leu Ser Ser Thr Leu Glu 155 160
Ala Pro Leu Leu Phe 165	Ser Lys Gln Asn Val 170	Val Ile Gly Ala Leu Ser 175
Ile Ile Tyr Pro Leu Tyr 180	Met Gly Gly Ala Arg Phe Thr 185	Met Val Arg 190
Ile Ala Asp Leu Met Gln Lys 195	Asp Ala Asn Glu Val Tyr Arg 200 205	Leu Lys
Lys Leu Ser Thr Phe Gln Glu 210 215	Leu Val Ser Val Tyr Tyr Gly Met Val 220	
Leu Asn Ala Glu Val Ala Glu Thr 225 230	Leu Glu Glu Val Glu Lys Gly His 235 240	
Tyr Lys His Phe Gln Asn Ala Leu Lys 245	Met Gln Lys Val Gly Gln Ile 250 255	
Ala Arg Val Glu Thr Leu Gly Ala Gln 260 265	Val Ala Tyr Asp Lys Ala His 270	
Ile Ala Ser Val Lys Ala Lys Asp 275 280	Val Leu Glu Val Ser Gln Leu Ser 285	
Phe Asn Ser Ile Leu Ser Ser Lys 290 295	Asp Asp Leu Val Pro Ser Ser Lys 300	
Leu Glu Ile Arg Thr Glu Lys Asn Leu 305 310	Pro Asp Leu Ser Phe Phe Val 315 320	
Ser Ser Thr Leu Asn Ser Tyr Pro Val 325 330	Leu Lys Thr Leu Glu Asn Gln 335	
Ile Gln Ile Ser Lys Glu Asn Thr Lys 340 345	Leu Gln Ile Ala Lys Phe Leu 350	
Pro Gln Val Ser Phe Phe Gly Ser 355 360	Tyr Ile Met Lys Gln Asn Asn Ser 365	
Val Phe Glu Asp Met Ile Pro Ser Trp 370 375	Phe Val Gly Val Ala Gly Arg 380	
Met Pro Ile Leu Ser Pro Thr Gly Arg 385 390	Ile Gln Lys Tyr Gln Ala Ser 395 400	
Lys Leu Ala Glu Leu Gln Val Ser Ser 405 410	Glu Gln Ile Gln Ala Lys Lys 415	
Asn Met Glu Leu Leu Val Asn Lys Thr 420 425	Tyr Lys Glu Thr Leu Ser Tyr 430	
Leu Lys Glu Tyr Lys Ser Leu Leu Ser 435 440	Ser Val Glu Leu Ala Lys Glu 445	

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D



Asn Leu Lys Leu Gln Glu Gln Ala Phe Leu Gln Gly Leu Ser Thr Asn  
 450 455 460

Ala Gln Val Ile Asp Ala Arg Asn Thr Leu Ser Ser Ile Val Val Glu  
 465 470 475 480

Gln Lys Ser Val Ala Tyr Lys Tyr Ile Val Ser Leu Ala Asn Leu Met  
 485 490 495

Ala Leu Ser Asp His Ile Asp Leu Phe Tyr Glu Phe Val Tyr \*  
 500 505 510

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS074

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG TTA AGT AGA GAC ATT GTC CAA TAT TCC AAG ATC CGC ACC GAG TTA	48
Met Leu Ser Arg Asp Ile Val Gln Tyr Ser Lys Ile Arg Thr Glu Leu	
515 520 525	
TAC GCT TAT CTT ACC TAT TTG TTT TCG CAC AAT ATC CGC AAC CAC CTC	96
Tyr Ala Tyr Leu Thr Tyr Leu Phe Ser His Asn Ile Arg Asn His Leu	
530 535 540	
CCT GAA ATC ACT TTG GAT TAT TTA AAC AAA CAG ATC AGA AAA ATG CAC	144
Pro Glu Ile Thr Leu Asp Tyr Leu Asn Lys Gln Ile Arg Lys Met His	
545 550 555	
GCT GAA ATC AAA ATG GCA AAA AAT TTT TTT GTG TTA GAC GCT AAG GGC	192
Ala Glu Ile Lys Met Ala Lys Asn Phe Phe Val Leu Asp Ala Lys Gly	
560 565 570 575	
ATG CTA ATT CTT AAG CCA AGC CAG CTT AAA GAG CAG GGG CAT AAG GAA	240
Met Leu Ile Leu Lys Pro Ser Gln Leu Lys Glu Gln Gly His Lys Glu	
580 585 590	
GGG ATA TTA GAG CAT GAT TTA ACA GAA GGG ATT GAA CTA GAA TCG CAT	288
Gly Ile Leu Glu His Asp Leu Thr Glu Gly Ile Glu Leu Glu Ser His	
595 600 605	
GCC AGT TTT AGC GAT AAG TAT TAT TTT TAT CAA GCC GTG AGC GAA AAG	336
Ala Ser Phe Ser Asp Lys Tyr Tyr Phe Tyr Gln Ala Val Ser Glu Lys	
610 615 620	

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CGT TGC ATT TTA ACG GAC CCC TAT CCT TCT AAA AAA GGA AAC CAT TTA 384  
 Arg Cys Ile Leu Thr Asp Pro Tyr Pro Ser Lys Lys Gly Asn His Leu  
 625 630 635

GTA GTG AGC GCG TCT TAC CCG GTG TAT GAT CAA AAT AAC GAT CTA GCG 432  
 Val Val Ser Ala Ser Tyr Pro Val Tyr Asp Gln Asn Asn Asp Leu Ala  
 640 645 650 655

TTT GTG GTG TGC TTG CAA ATC CCT TTG AGG GTA GCG ATT GAA ATC AGC 480  
 Phe Val Val Cys Leu Gln Ile Pro Leu Arg Val Ala Ile Glu Ile Ser  
 660 665 670

TCG CCT TCA AAG TAT TTC AGA ACC TTT AGC GAA GGG AGC ATG GTT ATG 528  
 Ser Pro Ser Lys Tyr Phe Arg Thr Phe Ser Glu Gly Ser Met Val Met  
 675 680 685

TAT TTT ATG ATT TCT ATC ATG CTC ACT TTA GTG TCG TTG CTT TTA TTT 576  
 Tyr Phe Met Ile Ser Ile Met Leu Thr Leu Val Ser Leu Leu Leu Phe  
 690 695 700

GTG AAA TGC ATT TCT AGC TTT TGG ACA GCG ATT GTT AAT TTT AGC AGT 624  
 Val Lys Cys Ile Ser Ser Phe Trp Thr Ala Ile Val Asn Phe Ser Ser  
 705 710 715

TTT GAC ATT AAA GAA GTG TTC CAC CCC ATT GTG CTT TTA ACC CTA GCC 672  
 Phe Asp Ile Lys Glu Val Phe His Pro Ile Val Leu Leu Thr Leu Ala  
 720 725 730 735

TTA GCC ACC TTT GAT CTA GTC AAG GCG ATT TTT GAA GAG GAA GTT TTG 720  
 Leu Ala Thr Phe Asp Leu Val Lys Ala Ile Phe Glu Glu Glu Val Leu  
 740 745 750

GGT AAA AAT AGC GGG GAC AAC CAC CAT GCG ATC CAC CGC ACG ATG ATC 768  
 Gly Lys Asn Ser Gly Asp Asn His His Ala Ile His Arg Thr Met Ile  
 755 760 765

AGG TTT TTA GGC TCT ATC ATT ATC GCA TTA GCC ATT GAA GCG TTA ATG 816  
 Arg Phe Leu Gly Ser Ile Ile Ile Ala Leu Ala Ile Glu Ala Leu Met  
 770 775 780

TTA GTG TTT AAA TTC AGC GTG AGC GAA CCG GAT AAA ATC ACT TAT GCG 864  
 Leu Val Phe Lys Phe Ser Val Ser Glu Pro Asp Lys Ile Thr Tyr Ala  
 785 790 795

GTG TAT TTG GCT GTT GGC GTG GCG GTG CTT TTG ATC AGT TTG GCG ATT 912  
 Val Tyr Leu Ala Val Gly Val Ala Val Leu Leu Ile Ser Leu Ala Ile  
 800 805 810 815

TAT GTC AAA TTC GCC TAT AGC GTG TTG CCC AAA CGA GAA CGC TAA 957  
 Tyr Val Lys Phe Ala Tyr Ser Val Leu Pro Lys Arg Glu Arg \*  
 820 825 830

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 Amino acids  
 (B) TYPE: Amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Leu Ser Arg Asp Ile Val Gln Tyr Ser Lys Ile Arg Thr Glu Leu  
 1 5 10 15  
 Tyr Ala Tyr Leu Thr Tyr Leu Phe Ser His Asn Ile Arg Asn His Leu  
 20 25 30  
 Pro Glu Ile Thr Leu Asp Tyr Leu Asn Lys Gln Ile Arg Lys Met His  
 35 40 45  
 Ala Glu Ile Lys Met Ala Lys Asn Phe Phe Val Leu Asp Ala Lys Gly  
 50 55 60  
 Met Leu Ile Leu Lys Pro Ser Gln Leu Lys Glu Gln Gly His Lys Glu  
 65 70 75 80  
 Gly Ile Leu Glu His Asp Leu Thr Glu Gly Ile Glu Leu Glu Ser His  
 85 90 95  
 Ala Ser Phe Ser Asp Lys Tyr Tyr Phe Tyr Gln Ala Val Ser Glu Lys  
 100 105 110  
 Arg Cys Ile Leu Thr Asp Pro Tyr Pro Ser Lys Lys Gly Asn His Leu  
 115 120 125  
 Val Val Ser Ala Ser Tyr Pro Val Tyr Asp Gln Asn Asn Asp Leu Ala  
 130 135 140  
 Phe Val Val Cys Leu Gln Ile Pro Leu Arg Val Ala Ile Glu Ile Ser  
 145 150 155 160  
 Ser Pro Ser Lys Tyr Phe Arg Thr Phe Ser Glu Gly Ser Met Val Met  
 165 170 175  
 Tyr Phe Met Ile Ser Ile Met Leu Thr Leu Val Ser Leu Leu Leu Phe  
 180 185 190  
 Val Lys Cys Ile Ser Ser Phe Trp Thr Ala Ile Val Asn Phe Ser Ser  
 195 200 205  
 Phe Asp Ile Lys Glu Val Phe His Pro Ile Val Leu Leu Thr Leu Ala  
 210 215 220  
 Leu Ala Thr Phe Asp Leu Val Lys Ala Ile Phe Glu Glu Glu Val Leu  
 225 230 235 240  
 Gly Lys Asn Ser Gly Asp Asn His His Ala Ile His Arg Thr Met Ile  
 245 250 255  
 Arg Phe Leu Gly Ser Ile Ile Ile Ala Leu Ala Ile Glu Ala Leu Met  
 260 265 270  
 Leu Val Phe Lys Phe Ser Val Ser Glu Pro Asp Lys Ile Thr Tyr Ala  
 275 280 285

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Val Tyr Leu Ala Val Gly Val Ala Val Leu Leu Ile Ser Leu Ala Ile  
 290 295 300

Tyr Val Lys Phe Ala Tyr Ser Val Leu Pro Lys Arg Glu Arg \*  
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS083

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG CAC TCT CCA AAT TTA GAA AAA GAA GAA ACC GAA ATC ATA GAA ACA	48
Met His Ser Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr	
320 325 330 335	
CTC CTT ATG CGT GAA AAA ATG CGT TTA TGC CCC TTG TAT TGG CGC ATC	96
Leu Leu Met Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile	
340 345 350	
TTA GCG TTT TTA ACC GAT GGT TTG TTA GTG GCG TTT TTA TTG AGC GAT	144
Leu Ala Phe Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp	
355 360 365	
CTT TTA GAC GCA TGC GAT TTC TTG CAT TCT TTA TAT TGG CTA GCT AAC	192
Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn	
370 375 380	
CCT ATT TAT CAC AGC GCA TTT GTT GCG ATG GGT TTT ATC ATC TTG TAT	240
Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr	
385 390 395	
GGC GTT TAT GAA ATC TTT TTT GTG TGT TTG TGC AAG ATG AGC TTG GCT	288
Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala	
400 405 410 415	
AAA CTG GTT TTT AGG ATT AAG ATT ATT GAT ATT TAT TTG GCA GAT TGC	336
Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys	
420 425 430	
CCC AGT AGG GCT ATT TTA TTG AAG CGT TTA GGG TTA AAG ATC GTG GTT	384
Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val	
435 440 445	
TTT CTA TGC CCC TTT TTA TGG TTT GTT GCG TTT AAA AAC CCC TAT CAT	432

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Phe Leu Cys Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His  
 450 455 460

AGG GCG TGG CAT GAA GAA AAA AGC AAA AGT CTT TTG GTA TTG TTT TAA 480  
 Arg Ala Trp His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe \*  
 465 470 475

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met His Ser Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr  
 1 5 10 15  
 Leu Leu Met Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile  
 20 25 30  
 Leu Ala Phe Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp  
 35 40 45  
 Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn  
 50 55 60  
 Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr  
 65 70 75 80  
 Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala  
 85 90 95  
 Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys  
 100 105 110  
 Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val  
 115 120 125  
 Phe Leu Cys Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His  
 130 135 140  
 Arg Ala Trp His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe \*  
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1983 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

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## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS084

## (ix) FEATURES:

(A) NAME/KEY: CDS

(B) POSITION:1..1983

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG ATT TAT TGG TTG TAT TTG GCG GTC TTT TTT TTG TTG AGC GCA TTA	48
Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu	
165 170 175	
GAC GCT AAA GAA ATC GCT ATG CAA CGA TTT GAC AAA CAA AAC CAT AAG	96
Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys	
180 185 190	
ATT TTT GAA ATC CTT GCG GAT AAA GTG AGC GCT AAA GAC AAT GTG ATA	144
Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile	
195 200 205	
ACC GCA TCA GGG AAT GCG ATC TTA TTG AAT TAT GAT GTG TAT ATT CTA	192
Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu	
210 215 220	
GCG GAC AAG GTG CGT TAT GAC ACT AAA ACC AAA GAA GCG TTA TTA GAG	240
Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu	
225 230 235 240	
GGG AAT ATC AAG GTT TAT AGG GGC GAG GGT TTG CTC GTT AAA ACC GAT	288
Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp	
245 250 255	
TAC GTG AAA TTG AGT TTG AAT GAA AAA TAT GAA ATC ATT TTC CCC TTT	336
Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe	
260 265 270	
TAT GTC CAA GAC AGC GTG AGC GGG ATT TGG GTG AGC GCG GAT ATT GCC	384
Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala	
275 280 285	
AGC GGA AAG GAT CAA AAA TAT AAG GTT AAA AAC ATG AGC ACT TCA GGG	432
Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly	
290 295 300	
TGC AGC ATT GAT AAC CCC ATT TGG CAT GTC AAT GCG ACT TCA GGC TCA	480
Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser	
305 310 315 320	
TTC AAC ATG CAA AAA TCG CAT TTG TCT ATG TGG AAT CCT AAG ATC TAT	528
Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr	
325 330 335	
GTC GGT GAT ATT CCT GTA TTG TAT TTG CCC TAT ATT TTC ATG TCC ACG	576
Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr	
340 345 350	
AGC AAT AAA AGA ACT ACT GGG TTT TTA TAC CCT GAG TTT GGC ACT TCC	624

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Ser	Asn	Lys	Arg	Thr	Thr	Gly	Phe	Leu	Tyr	Pro	Glu	Phe	Gly	Thr	Ser	
	355						360					365				
AAC	TTA	GAC	GGC	TTT	ATT	TAT	TTG	CAA	CCC	TTT	TAT	TTA	GCC	CCC	AAA	672
Asn	Leu	Asp	Gly	Phe	Ile	Tyr	Leu	Gln	Pro	Phe	Tyr	Leu	Ala	Pro	Lys	
	370					375					380					
AAC	TCA	TGG	GAT	ATG	ACC	TTT	ACC	CCA	CAA	ATC	CGC	TAT	AAA	AGG	GGT	720
Asn	Ser	Trp	Asp	Met	Thr	Phe	Thr	Pro	Gln	Ile	Arg	Tyr	Lys	Arg	Gly	
	385				390					395					400	
TTT	GGC	TTG	AAT	TTT	GAA	GCG	CGC	TAC	ATT	AAC	TCT	AAA	AAC	GAC	AGG	768
Phe	Gly	Leu	Asn	Phe	Glu	Ala	Arg	Tyr	Ile	Asn	Ser	Lys	Asn	Asp	Arg	
			405					410						415		
TTT	TTA	TTC	AAC	GCG	CGC	TAT	TTT	AGG	AAT	TAC	ACC	CAA	TAT	GTC	AAA	816
Phe	Leu	Phe	Asn	Ala	Arg	Tyr	Phe	Arg	Asn	Tyr	Thr	Gln	Tyr	Val	Lys	
			420					425					430			
CGC	TAC	GAT	TTG	AGG	AAT	CAA	AAT	ATC	TAC	GGG	TTT	GAA	TTT	TTA	AGC	864
Arg	Tyr	Asp	Leu	Arg	Asn	Gln	Asn	Ile	Tyr	Gly	Phe	Glu	Phe	Leu	Ser	
		435					440					445				
TCT	AGC	AGG	GAC	ACT	TTA	CAA	AAA	TAC	TTC	CAC	CTT	AAG	TCT	AAT	ATT	912
Ser	Ser	Arg	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	His	Leu	Lys	Ser	Asn	Ile	
	450					455					460					
GAC	AAC	GGG	CAT	TAC	ATT	GAC	TTT	TTA	TAC	ATG	AAC	GAT	TTG	GAC	TAT	960
Asp	Asn	Gly	His	Tyr	Ile	Asp	Phe	Leu	Tyr	Met	Asn	Asp	Leu	Asp	Tyr	
	465				470				475					480		
GTG	CGT	TTT	GAA	AAG	GTT	AAT	AAG	CGT	ATC	ACA	GAC	GCC	ACG	CAC	ATG	1008
Val	Arg	Phe	Glu	Lys	Val	Asn	Lys	Arg	Ile	Thr	Asp	Ala	Thr	His	Met	
			485					490					495			
TCT	AGG	GCG	AAT	TAC	TAT	TTG	CAA	ACA	GAA	AAC	AAT	TAT	TAC	GGC	TTG	1056
Ser	Arg	Ala	Asn	Tyr	Tyr	Leu	Gln	Thr	Glu	Asn	Asn	Tyr	Tyr	Gly	Leu	
			500					505					510			
AAT	ATC	AAG	TAT	TTT	TTA	AAC	CTG	AAT	AAA	ATC	AAC	AAT	AAC	CGC	ACT	1104
Asn	Ile	Lys	Tyr	Phe	Leu	Asn	Leu	Asn	Lys	Ile	Asn	Asn	Asn	Arg	Thr	
		515					520					525				
TTC	CAA	TCT	GTC	CCT	AAT	TTG	CAA	TAC	CAT	AAA	TAT	TTA	AAT	TCT	TTG	1152
Phe	Gln	Ser	Val	Pro	Asn	Leu	Gln	Tyr	His	Lys	Tyr	Leu	Asn	Ser	Leu	
	530					535					540					
TAT	TTT	AGA	AAT	TTG	TTG	TAT	TCG	GTG	GAT	TAT	CAG	TTT	AGA	AAC	ACC	1200
Tyr	Phe	Arg	Asn	Leu	Leu	Tyr	Ser	Val	Asp	Tyr	Gln	Phe	Arg	Asn	Thr	
	545				550				555					560		
GCA	AGA	GAG	ATT	GGT	TAT	GGC	TAT	GTG	CAA	AAC	GCT	TTG	AAT	GTG	CCG	1248
Ala	Arg	Glu	Ile	Gly	Tyr	Gly	Tyr	Val	Gln	Asn	Ala	Leu	Asn	Val	Pro	
			565					570					575			
GTG	GGC	TTG	CAA	TTT	TCT	TTG	TTT	AAA	AAG	TAT	TTG	TCT	TTA	GGG	CTT	1296
Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Lys	Tyr	Leu	Ser	Leu	Gly	Leu	
			580					585					590			

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TGG AAT GAT CTC CAA CTA TCT AAT GTG GCT TTA ATG CAA TCT AAA AAT Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn 595 600 605	1344
TCC TTC GTG CCT ACG ATC CCT AAT GAA TCA AGG GAA TTT GGG AAT TTT Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe 610 615 620	1392
GTG TCT TCA AAT TTT TCC ATG TAT GTC AAT ACG GAT TTG GCT AGA GAA Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu 625 630 635 640	1440
TAC AAC AAG CTT TTC CAC ACG ATC CAA CTA GAA GCG ATT TTC AAC ATC Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile 645 650 655	1488
CCT TAT TAC ACC TTT AAA AAC GGC TTA TTT TCT CAA AAC ATG TAT GCT Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala 660 665 670	1536
TTA AGC GCG CAA GCC TTA AAC AGC TAC ACT TCG CCT TTA TTG AGA GAT Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp 675 680 685	1584
TAT GAT TAT CAA GGG CGT TTG TAT GAC TCG GTG TGG AAT CCT AGC AGT Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser 690 695 700	1632
ATT TTA CCT AGC AAT GCG AGC AAC AAG ACG GTG GAT TTA ACC CTA ACG Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr 705 710 715 720	1680
CAA TAC CTT TAT GGC TTA GGG GGG CAA GAG TTA TTG TAT TTT AAA ATA Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile 725 730 735	1728
TCG CAA CTC ATC AAT CTT GAC GAT AAA GTT TCG CCC TTT AGA ATG CCA Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro 740 745 750	1776
CTA GAG AGC AAG ATC GGG TTT TCG CCC TTA ACG GGA TTG AAC ATC TTT Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe 755 760 765	1824
GGG AAT GTC TTT TAT TCG TTT TAT CAA AAC CGC TTA GAA GAA ATC TCT Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser 770 775 780	1872
GTG AAC GCC AAT TAC CAA CGC AAG TTT TTA AGC TTT AAC CTC TCT TAT Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr 785 790 795 800	1920
TTT TTA AAA AAC AAT TTT AGC AGT GGG ATT AAT AGC ATT GTA GAA AAT Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn 805 810 815	1968
CTG CGG ATT ATT TAA Leu Arg Ile Ile *	1983
820	

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## (2) INFORMATION FOR SEQ ID NO: 26:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 661 Amino acids

(B) TYPE: Amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu  
 1 5 10 15

Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys  
 20 25 30

Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile  
 35 40 45

Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu  
 50 55 60

Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu  
 65 70 75 80

Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp  
 85 90 95

Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe  
 100 105 110

Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala  
 115 120 125

Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly  
 130 135 140

Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser  
 145 150 155 160

Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr  
 165 170 175

Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr  
 180 185 190

Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser  
 195 200 205

Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys  
 210 215 220

Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg Tyr Lys Arg Gly  
 225 230 235 240

Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg  
 245 250 255

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D

Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys  
 260 265 270  
 Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser  
 275 280 285  
 Ser Ser Arg Asp Thr Leu Gln Lys Tyr Phe His Leu Lys Ser Asn Ile  
 290 295 300  
 Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr  
 305 310 315 320  
 Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr His Met  
 325 330 335  
 Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu  
 340 345 350  
 Asn Ile Lys Tyr Phe Leu Asn Leu Asn Lys Ile Asn Asn Asn Arg Thr  
 355 360 365  
 Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu  
 370 375 380  
 Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr  
 385 390 395 400  
 Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn Val Pro  
 405 410 415  
 Val Gly Leu Gln Phe Ser Leu Phe Lys Lys Tyr Leu Ser Leu Gly Leu  
 420 425 430  
 Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn  
 435 440 445  
 Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe  
 450 455 460  
 Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu  
 465 470 475 480  
 Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile  
 485 490 495  
 Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala  
 500 505 510  
 Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp  
 515 520 525  
 Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser  
 530 535 540  
 Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr  
 545 550 555 560  
 Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile

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D

565                      570                      575  
 Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro  
                          580                      585                      590  
 Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe  
                          595                      600                      605  
 Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser  
                          610                      615                      620  
 Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr  
                          625                      630                      635                      640  
 Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn  
                          645                      650                      655  
 Leu Arg Ile Ile \*  
                          660

## (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPC085

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..372

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG CGT TTG TTT ATC TCA CTA GTT TTG TTT TGG TGG TGG TTA AGT TTG	48
Met Arg Leu Phe Ile Ser Leu Val Leu Phe Trp Trp Trp Leu Ser Leu	
665                      670                      675	
AAC GCT AAA GAA GCG GAT TTC ATC TCT GAT TTG GAA TAC GGG ATG GCT	96
Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu Tyr Gly Met Ala	
680                      685                      690	
CTT TAT AAA AAC CCT AGG GGT GTT GCG TGC GCG AAA TGC CAT GGC ATT	144
Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys Cys His Gly Ile	
695                      700                      705	
AAA GGC GAA CAA CAA GAA ATC ACT TTT TAT TAT GAA AAA GGC GAA AAA	192
Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu Lys Gly Glu Lys	
710                      715                      720                      725	
AAA ATC CTC TAC GCC CCT AAA ATC AAC CAT TTA GAT TTT AAA ACC TTT	240
Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp Phe Lys Thr Phe	
730                      735                      740	

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AAA GAC GCC CTG AGT TTA GGC AAA GGC ATG ATG CCT AAA TAC AAT CTC 288  
 Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro Lys Tyr Asn Leu  
           745                               750                               755

AAT TTA GAA GAA ATC CAA GCG ATT TAC CTT TAC ATC ACC TCT TTA GAG 336  
 Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile Thr Ser Leu Glu  
           760                               765                               770

CAT AAA GAC GAG CAT AAG AAT CCT TCC AAG CCT TAA 372  
 His Lys Asp Glu His Lys Asn Pro Ser Lys Pro \*  
           775                               780                               785

## (2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Arg Leu Phe Ile Ser Leu Val Leu Phe Trp Trp Trp Leu Ser Leu  
   1                              5                              10                              15

Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu Tyr Gly Met Ala  
           20                              25                              30

Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys Cys His Gly Ile  
           35                              40                              45

Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu Lys Gly Glu Lys  
           50                              55                              60

Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp Phe Lys Thr Phe  
           65                              70                              75                              80

Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro Lys Tyr Asn Leu  
           85                              90                              95

Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile Thr Ser Leu Glu  
           100                              105                              110

His Lys Asp Glu His Lys Asn Pro Ser Lys Pro \*  
           115                              120

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 558 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

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(B) CLONE(S) : HPC090

## (ix) FEATURES:

(A) NAME/KEY: CDS

(B) POSITION:1..558

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG CGT TGG TGG TGT TTT TTG GTG TGT TGT TTT GGT ATT TTA AGC GTG 48  
 Met Arg Trp Trp Cys Phe Leu Val Cys Cys Phe Gly Ile Leu Ser Val  
 125 130 135 140

ATG GAC GCT CAA AAA ACA GAC AAT AAA GGT TTG AAA AAA GAA AGA GAA 96  
 Met Asp Ala Gln Lys Thr Asp Asn Lys Gly Leu Lys Lys Glu Arg Glu  
 145 150 155

CTT TTA GAA ATT ACT GGC AAC CAA TTT GTA GCG AAC GAC AAA ACC AAA 144  
 Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp Lys Thr Lys  
 160 165 170

ACC GCC GTT ATT CAA GGC AAT GTG CAG ATC AAA AAA GGT AAA GAC CGG 192  
 Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly Lys Asp Arg  
 175 180 185

TTG TTT GCG GAT AAG GTG AGC GTG TTT TTA AAC GAT AAA CGA AAG CCA 240  
 Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys Arg Lys Pro  
 190 195 200

GAG CGC TAT GAA GCC ACA GGG AAC ACG CAT TTT AAC ATC TTT ACA GAG 288  
 Glu Arg Tyr Glu Ala Thr Gly Asn Thr His Phe Asn Ile Phe Thr Glu  
 205 210 215 220

GAC AAT CGT GAA ATC AGC GGG AGC GCT GAC AAG CTC ATT TAT AAC GCA 336  
 Asp Asn Arg Glu Ile Ser Gly Ser Ala Asp Lys Leu Ile Tyr Asn Ala  
 225 230 235

TTG AAT GGG GAA TAC AAA TTA TTG CAA AAT GCG GTG GTT AGA GAA GTG 384  
 Leu Asn Gly Glu Tyr Lys Leu Leu Gln Asn Ala Val Val Arg Glu Val  
 240 245 250

GGG AAA TCT AAT GTC ATC ACT GGC GAT GAA ATC ATT TTA AAC AAA ACT 432  
 Gly Lys Ser Asn Val Ile Thr Gly Asp Glu Ile Ile Leu Asn Lys Thr  
 255 260 265

AAG GGT TAT GCT GAT GTG TTA GGG AGC GCG AAA CGG CCC GCT AAA TTC 480  
 Lys Gly Tyr Ala Asp Val Leu Gly Ser Ala Lys Arg Pro Ala Lys Phe  
 270 275 280

GTG TTT GAT ATG GAA GAT ATT AAT GAA GAA AAT CGT AAG GCT AAA TTG 528  
 Val Phe Asp Met Glu Asp Ile Asn Glu Glu Asn Arg Lys Ala Lys Leu  
 285 290 295 300

AAG AAG AAA GGC ACT AAG GAA AAA CCA TGA 558  
 Lys Lys Lys Gly Thr Lys Glu Lys Pro \*  
 305 310

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 186 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Arg Trp Trp Cys Phe Leu Val Cys Cys Phe Gly Ile Leu Ser Val  
 1 5 10 15  
 Met Asp Ala Gln Lys Thr Asp Asn Lys Gly Leu Lys Lys Glu Arg Glu  
 20 25 30  
 Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp Lys Thr Lys  
 35 40 45  
 Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly Lys Asp Arg  
 50 55 60  
 Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys Arg Lys Pro  
 65 70 75 80  
 Glu Arg Tyr Glu Ala Thr Gly Asn Thr His Phe Asn Ile Phe Thr Glu  
 85 90 95  
 Asp Asn Arg Glu Ile Ser Gly Ser Ala Asp Lys Leu Ile Tyr Asn Ala  
 100 105 110  
 Leu Asn Gly Glu Tyr Lys Leu Leu Gln Asn Ala Val Val Arg Glu Val  
 115 120 125  
 Gly Lys Ser Asn Val Ile Thr Gly Asp Glu Ile Ile Leu Asn Lys Thr  
 130 135 140  
 Lys Gly Tyr Ala Asp Val Leu Gly Ser Ala Lys Arg Pro Ala Lys Phe  
 145 150 155 160  
 Val Phe Asp Met Glu Asp Ile Asn Glu Glu Asn Arg Lys Ala Lys Leu  
 165 170 175  
 Lys Lys Lys Gly Thr Lys Glu Lys Pro \*

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 768 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS104

(ix) FEATURES:

09080115 113001

(A) NAME/KEY: CDS  
(B) POSITION:1..768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GAT ATT TAT GCG TTA TAT ATA GCG ATA GGG CTT TTT ACT GGC ATT	48
Met Asp Ile Tyr Ala Leu Tyr Ile Ala Ile Gly Leu Phe Thr Gly Ile	
190 195 200	
CTA TCA GGG ATT TTT GGC ATT GGT GGG GGG TTG ATC ATT GTC CCT ATC	96
Leu Ser Gly Ile Phe Gly Ile Gly Gly Gly Leu Ile Ile Val Pro Ile	
205 210 215	
ATG CTC GCA ACC GGG CAT TCT TTT GAA GAA TCC ATT GGG ATT TCC ATT	144
Met Leu Ala Thr Gly His Ser Phe Glu Glu Ser Ile Gly Ile Ser Ile	
220 225 230	
TTG CAA ATG GCG CTT TCA TCG TTC GTG GGC TCT GTT TTG AAT TTC AAA	192
Leu Gln Met Ala Leu Ser Ser Phe Val Gly Ser Val Leu Asn Phe Lys	
235 240 245 250	
AAA AAA TCG CTT GAT TTT TCT TTA GGC TTG TTG ATA GGG GCA GGG GGG	240
Lys Lys Ser Leu Asp Phe Ser Leu Gly Leu Leu Ile Gly Ala Gly Gly	
255 260 265	
CTG ATA GGG GCG AGT TTT AGC GGA TTT GTT TTA AAA ATC GTT TCC AGT	288
Leu Ile Gly Ala Ser Phe Ser Gly Phe Val Leu Lys Ile Val Ser Ser	
270 275 280	
AAA ATT TTA ATG GTT ATT TTC GCG CTT TTA GTC GTG TAT TCT ATG ATC	336
Lys Ile Leu Met Val Ile Phe Ala Leu Leu Val Val Tyr Ser Met Ile	
285 290 295	
CAA TTT GTT TTG AAA CCC AAA AAA AAA GAT TTG ATA GCG GAT ACT AAA	384
Gln Phe Val Leu Lys Pro Lys Lys Lys Asp Leu Ile Ala Asp Thr Lys	
300 305 310	
CGC TAT CAT CTG CAA GGT TTG AAA TTA TTT TTA ATT GGC ACG CTC ACA	432
Arg Tyr His Leu Gln Gly Leu Lys Leu Phe Leu Ile Gly Thr Leu Thr	
315 320 325 330	
GGG TTT TTT GCT ATC ACT TTA GGG ATT GGT GGG GGG ATG CTC ATG GTG	480
Gly Phe Phe Ala Ile Thr Leu Gly Ile Gly Gly Gly Met Leu Met Val	
335 340 345	
CCT TTG ATG CAT TAT TTT TTA GGG TAT GAT TCT AAA AAA TGC GTG GCT	528
Pro Leu Met His Tyr Phe Leu Gly Tyr Asp Ser Lys Lys Cys Val Ala	
350 355 360	
CTA GGG TTA TTT TTC ATC TTG TTT TCT TCT ATT TCA GGA GCT TTT TCT	576
Leu Gly Leu Phe Phe Ile Leu Phe Ser Ser Ile Ser Gly Ala Phe Ser	
365 370 375	
TTA ATG TAT CAC CAC ATC ATC AAT AAA GAA GTG CTC TTA GCA GGG GCG	624
Leu Met Tyr His His Ile Ile Asn Lys Glu Val Leu Leu Ala Gly Ala	
380 385 390	
ATT GTG GGA TTA GGA TCT GTT ATG GGC GTG AGC ATT GGG ATT AAA TGG	672

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Ile Val Gly Leu Gly Ser Val Met Gly Val Ser Ile Gly Ile Lys Trp  
395 400 405 410

ATC ATG GGG CTT TTG AAT GAA AAA ATG CAT AAA GCT TTG ATT TTA GGG 720  
Ile Met Gly Leu Leu Asn Glu Lys Met His Lys Ala Leu Ile Leu Gly  
415 420 425

GTG TAT GGT TTG TCG CTA TTG ATT GTT TTA TAC AAA CTC TTT TTT TAA 768  
Val Tyr Gly Leu Ser Leu Leu Ile Val Leu Tyr Lys Leu Phe Phe \*  
430 435 440

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Asp Ile Tyr Ala Leu Tyr Ile Ala Ile Gly Leu Phe Thr Gly Ile  
1 5 10 15  
Leu Ser Gly Ile Phe Gly Ile Gly Gly Gly Leu Ile Ile Val Pro Ile  
20 25 30  
Met Leu Ala Thr Gly His Ser Phe Glu Glu Ser Ile Gly Ile Ser Ile  
35 40 45  
Leu Gln Met Ala Leu Ser Ser Phe Val Gly Ser Val Leu Asn Phe Lys  
50 55 60  
Lys Lys Ser Leu Asp Phe Ser Leu Gly Leu Leu Ile Gly Ala Gly Gly  
65 70 75 80  
Leu Ile Gly Ala Ser Phe Ser Gly Phe Val Leu Lys Ile Val Ser Ser  
85 90 95  
Lys Ile Leu Met Val Ile Phe Ala Leu Val Val Tyr Ser Met Ile  
100 105 110  
Gln Phe Val Leu Lys Pro Lys Lys Lys Asp Leu Ile Ala Asp Thr Lys  
115 120 125  
Arg Tyr His Leu Gln Gly Leu Lys Leu Phe Leu Ile Gly Thr Leu Thr  
130 135 140  
Gly Phe Phe Ala Ile Thr Leu Gly Ile Gly Gly Gly Met Leu Met Val  
145 150 155 160  
Pro Leu Met His Tyr Phe Leu Gly Tyr Asp Ser Lys Lys Cys Val Ala  
165 170 175  
Leu Gly Leu Phe Phe Ile Leu Phe Ser Ser Ile Ser Gly Ala Phe Ser  
180 185 190  
Leu Met Tyr His His Ile Ile Asn Lys Glu Val Leu Leu Ala Gly Ala

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195	200	205
Ile Val Gly Leu Gly Ser Val Met Gly Val Ser Ile Gly Ile Lys Trp		
210	215	220
Ile Met Gly Leu Leu Asn Glu Lys Met His Lys Ala Leu Ile Leu Gly		
225	230	235 240
Val Tyr Gly Leu Ser Leu Leu Ile Val Leu Tyr Lys Leu Phe Phe *		
245	250	255

## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2367 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS115

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..2367

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATG AAA TGT TCG CAT TGC CAG TTG GAG TTT AAA GAA AGT GAG CTT TTT	48
Met Lys Cys Ser His Cys Gln Leu Glu Phe Lys Glu Ser Glu Leu Phe	
260 265 270	
AAA GAG GTG ATC AAT CAT AAA GAA TTG CAT TTT TGC TGC ACG GGG TGC	96
Lys Glu Val Ile Asn His Lys Glu Leu His Phe Cys Cys Thr Gly Cys	
275 280 285	
GCT AGG GTG TAT GCG TTA TTG TTA GAT TTG AAT TTA GAG AGC TTT TAT	144
Ala Arg Val Tyr Ala Leu Leu Leu Asp Leu Asn Leu Glu Ser Phe Tyr	
290 295 300	
GAC AAA TTA AAC GAT TCC ACT TTA GCC CCC GTA ACG CCC CAA GAT TCA	192
Asp Lys Leu Asn Asp Ser Thr Leu Ala Pro Val Thr Pro Gln Asp Ser	
305 310 315 320	
ATG AGC GCT TTG GAA TTA GAA CAA GCC CTT GAA GAA AAC AAT AAG GGC	240
Met Ser Ala Leu Glu Leu Glu Gln Ala Leu Glu Glu Asn Asn Lys Gly	
325 330 335	
GAT TTT ATC CTT AAT CTT TTG TTA GAA AAA ACG CAT TGT AAC GCT TGC	288
Asp Phe Ile Leu Asn Leu Leu Leu Glu Lys Thr His Cys Asn Ala Cys	
340 345 350	
TTG TGG CTC AAT CAA AAG GTT TTA GAA CGT TTA AGT GGG GTT AAA AAA	336
Leu Trp Leu Asn Gln Lys Val Leu Glu Arg Leu Ser Gly Val Lys Lys	
355 360 365	

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GTG AGC GTG AAT TTC ACC ACC CAC CAC TTG CAA ATC GTG TTT GAG AAG Val Ser Val Asn Phe Thr Thr His His Leu Gln Ile Val Phe Glu Lys 370 375 380	384
TCC TTA AAC CCT AAA GAG ATT ATT CAA AAA ATT GAG AGT TTG GGC TAT Ser Leu Asn Pro Lys Glu Ile Ile Gln Lys Ile Glu Ser Leu Gly Tyr 385 390 395 400	432
GGG GCT AAA ATT TAT AAT GCG CAA AAT TAC ACC CTA AAA GCG CAA AAA Gly Ala Lys Ile Tyr Asn Ala Gln Asn Tyr Thr Leu Lys Ala Gln Lys 405 410 415	480
GAA CAG CGC TCC TAC TTG CTC ACT TTG AGC GTG GGG TTT TTT GCC ACT Glu Gln Arg Ser Tyr Leu Leu Thr Leu Ser Val Gly Phe Phe Ala Thr 420 425 430	528
ATG AAT TTG ATG TTT ATC GCC ATT GCC AAA TAC GCA AGT TAT GGT GGC Met Asn Leu Met Phe Ile Ala Ile Ala Lys Tyr Ala Ser Tyr Gly Gly 435 440 445	576
GCA AGT TAT GGC GGT GCG AAT TAT GGC GCT GGC ATG GAT AAG CTT ATG Ala Ser Tyr Gly Gly Ala Asn Tyr Gly Ala Gly Met Asp Lys Leu Met 450 455 460	624
CAA AGG AAT TTG GAT CTC GTA TCG CTC TTT TTA AGC TTG TTG GTG TTA Gln Arg Asn Leu Asp Leu Val Ser Leu Phe Leu Ser Leu Leu Val Leu 465 470 475 480	672
GTG GTT GTG GGG CGT TTT TTC ATT AAG GGG GCG TTT TAT GGG CTA AAA Val Val Val Gly Arg Phe Phe Ile Lys Gly Ala Phe Tyr Gly Leu Lys 485 490 495	720
AAT GGC GTT TTG GGC ATG GAT TTG AGC GTG TCT TTT GGA GCG TTA TCG Asn Gly Val Leu Gly Met Asp Leu Ser Val Ser Phe Gly Ala Leu Ser 500 505 510	768
GCG TTT GTT TAT TCC GTT TAT GCC ATG TTG GTG TCC CAA GAG ACT TAT Ala Phe Val Tyr Ser Val Tyr Ala Met Leu Val Ser Gln Glu Thr Tyr 515 520 525	816
TTT GAA GCG AGC AGC ACG ATT CTA ACG CTT GTT TTT GGC TCT AAG TTT Phe Glu Ala Ser Ser Thr Ile Leu Thr Leu Val Phe Gly Ser Lys Phe 530 535 540	864
TTG GAA TTA AAA GCC AGG CTG TTT GCG AAT GAA AAA TGT CTG GCC CTA Leu Glu Leu Lys Ala Arg Leu Phe Ala Asn Glu Lys Cys Leu Ala Leu 545 550 555 560	912
GAA TCG CAT GAA ATC CAT AGC GTG ATC GTT GTA GAA AAT GGC AAG CAA Glu Ser His Glu Ile His Ser Val Ile Val Val Glu Asn Gly Lys Gln 565 570 575	960
ACA GAA AAA CAC CCT AAA GAT GTG GCG ATA GGC TCT GTT GTT TGG GTG Thr Glu Lys His Pro Lys Asp Val Ala Ile Gly Ser Val Val Trp Val 580 585 590	1008
CCA AGC GGG GCT AAA ATC GCA CTA GAT GGC GTG CTT TTA AAT AAT GCG Pro Ser Gly Ala Lys Ile Ala Leu Asp Gly Val Leu Leu Asn Asn Ala	1056

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595	600	605	
AGC GTG GAT GCG TCT TTG ATC AGT GGG GAG TTT AAG CCT TTG GAA TTG Ser Val Asp Ala Ser Leu Ile Ser Gly Glu Phe Lys Pro Leu Glu Leu 610 615 620			1104
GGG GTT AAT GAT CCA ATT TTA GGG GGT TAT GTG AAT GTG GGC GTG CCT Gly Val Asn Asp Pro Ile Leu Gly Gly Tyr Val Asn Val Gly Val Pro 625 630 635 640			1152
TTT AGC TAT CAA GTG AGC GCT AAT TTT CAA AAC TCA CGC CTT TCT GGT Phe Ser Tyr Gln Val Ser Ala Asn Phe Gln Asn Ser Arg Leu Ser Gly 645 650 655			1200
TTG TTA GAA ACT TTA AAA AAG AGT TTT TTA GAA AAG CCC TTA ATT GAG Leu Leu Glu Thr Leu Lys Lys Ser Phe Leu Glu Lys Pro Leu Ile Glu 660 665 670			1248
AGT AGC GCG AAT CAA ATT GCG GAT ATT TTT TCT AAA GCG GTG TTG TTT Ser Ser Ala Asn Gln Ile Ala Asp Ile Phe Ser Lys Ala Val Leu Phe 675 680 685			1296
TTA GCC TTT GTA AGC TTT TTG TTA TGG CAA TTT GGT TTG GGG GGT AAT Leu Ala Phe Val Ser Phe Leu Leu Trp Gln Phe Gly Leu Gly Gly Asn 690 695 700			1344
TTT GAA AAA GCC TTA ATG GTG TGT ATT AGC GTG CTA GTC ATC AGC TGC Phe Glu Lys Ala Leu Met Val Cys Ile Ser Val Leu Val Ile Ser Cys 705 710 715 720			1392
CCT TGC GCG TTC GCT CTG GCT ACG CCC ATT GCG TTA GTG ATA GGG GTG Pro Cys Ala Phe Ala Leu Ala Thr Pro Ile Ala Leu Val Ile Gly Val 725 730 735			1440
TTT AAA AAC CCT TTG ATC GTG TTT AAA GAA GCG TTG TTT TTA GAA ACT Phe Lys Asn Pro Leu Ile Val Phe Lys Glu Ala Leu Phe Leu Glu Thr 740 745 750			1488
CTG GCT AAA GTG AAA AAA ATC TTT ATA GAC AAA ACC GGC ACG CTC ACG Leu Ala Lys Val Lys Lys Ile Phe Ile Asp Lys Thr Gly Thr Leu Thr 755 760 765			1536
CAA AAA GAA GTC CTT TTA AAA GAA AAA ATC ATT TAT GAA GAA TTT GAT Gln Lys Glu Val Leu Leu Lys Glu Lys Ile Ile Tyr Glu Glu Phe Asp 770 775 780			1584
GGA AGG CTT TTG AAG AGC CTT TTA AAA GTG AGA GAG CAT TTA GCC CAT Gly Arg Leu Leu Lys Ser Leu Leu Lys Val Arg Glu His Leu Ala His 785 790 795 800			1632
AGC GCG ATT CTT AAA TCT CTA GAT GGC GAT GAG GTT AGT TTA GAA AAG Ser Ala Ile Leu Lys Ser Leu Asp Gly Asp Glu Val Ser Leu Glu Lys 805 810 815			1680
ATA GAG TTT TTC GCT CAT GGT CTG AAA GCG AGC TAT CAA AAC GAA ACC Ile Glu Phe Phe Ala His Gly Leu Lys Ala Ser Tyr Gln Asn Glu Thr 820 825 830			1728
CTG CTA GTG GGG AGT TTG AAA TTT TTG GGA TCT ATG GGG GTG GAT ATA			1776

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Leu	Leu	Val	Gly	Ser	Leu	Lys	Phe	Leu	Gly	Ser	Met	Gly	Val	Asp	Ile	
		835					840					845				
CCA	ATG	AAA	GAG	AGC	GCT	AAT	ATC	ATG	GTA	GGC	TTT	GCG	AAA	AAT	GAG	1824
Pro	Met	Lys	Glu	Ser	Ala	Asn	Ile	Met	Val	Gly	Phe	Ala	Lys	Asn	Glu	
		850				855				860						
ACT	TTA	TGC	GCG	TTA	TTC	ATT	TTA	GAA	GAG	CGT	TTG	AAA	GCT	AAC	GCT	1872
Thr	Leu	Cys	Ala	Leu	Phe	Ile	Leu	Glu	Glu	Arg	Leu	Lys	Ala	Asn	Ala	
		865			870					875					880	
AAA	GAA	GTC	GTT	CAG	GCT	TTA	CAA	AAT	AAA	GGC	TTA	GAA	TTA	GAG	ATT	1920
Lys	Glu	Val	Val	Gln	Ala	Leu	Gln	Asn	Lys	Gly	Leu	Glu	Leu	Glu	Ile	
				885					890					895		
TTA	AGC	GGG	GAT	AAT	GAA	AGC	TCG	GTT	AAG	GAG	TGC	GCG	AAA	AAA	TTA	1968
Leu	Ser	Gly	Asp	Asn	Glu	Ser	Ser	Val	Lys	Glu	Cys	Ala	Lys	Lys	Leu	
			900					905						910		
GGG	ATT	TCT	AAT	TAT	CAT	GCC	CAT	TTG	ACC	CCT	GAA	GAT	AAG	GCT	CAA	2016
Gly	Ile	Ser	Asn	Tyr	His	Ala	His	Leu	Thr	Pro	Glu	Asp	Lys	Ala	Gln	
		915					920						925			
ACC	ATC	AGC	TCT	TAT	AAG	GGC	GTT	TGC	GCG	ATG	GTA	GGC	GAT	GGC	AAT	2064
Thr	Ile	Ser	Ser	Tyr	Lys	Gly	Val	Cys	Ala	Met	Val	Gly	Asp	Gly	Asn	
		930				935					940					
AAT	GAT	GCG	TTA	GCC	TTA	AAA	CAA	GCG	AGC	GTT	TCT	TTA	GGG	TTT	GAA	2112
Asn	Asp	Ala	Leu	Ala	Leu	Lys	Gln	Ala	Ser	Val	Ser	Leu	Gly	Phe	Glu	
		945			950					955					960	
AAA	AGC	GCT	TTG	AGT	AAA	AGC	GCA	TGC	GAT	ATT	TTG	CTT	TTA	GAA	GAG	2160
Lys	Ser	Ala	Leu	Ser	Lys	Ser	Ala	Cys	Asp	Ile	Leu	Leu	Leu	Glu	Glu	
				965				970						975		
GAT	TTG	AGT	TTG	CTA	AAA	AAA	GCG	TTT	GAT	AAC	GCT	CAA	AAA	GTC	TAT	2208
Asp	Leu	Ser	Leu	Leu	Lys	Lys	Ala	Phe	Asp	Asn	Ala	Gln	Lys	Val	Tyr	
			980					985						990		
CAA	GTG	GTG	TTG	CAA	AAC	ATT	GTT	TTG	AGC	TTG	ATT	TAT	AAC	GCT	ATT	2256
Gln	Val	Val	Leu	Gln	Asn	Ile	Val	Leu	Ser	Leu	Ile	Tyr	Asn	Ala	Ile	
		995					1000						1005			
TTA	ATC	CCG	GTC	GCT	ATG	CTA	GGA	TAC	ATT	AAC	CCT	TTA	ATA	GCG	AGT	2304
Leu	Ile	Pro	Val	Ala	Met	Leu	Gly	Tyr	Ile	Asn	Pro	Leu	Ile	Ala	Ser	
		1010				1015					1020					
TTG	AGC	ATG	AGC	GCT	AGC	TCA	CTC	TTA	GTG	GTC	TTA	AAT	TCT	TTG	AGG	2352
Leu	Ser	Met	Ser	Ala	Ser	Ser	Leu	Leu	Val	Val	Leu	Asn	Ser	Leu	Arg	
		1025			1030				1035					1040		
TTG	AAA	CGC	TCT	TAA												2367
Leu	Lys	Arg	Ser	*												
				1045												

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Lys Cys Ser His Cys Gln Leu Glu Phe Lys Glu Ser Glu Leu Phe  
 1 5 10 15  
 Lys Glu Val Ile Asn His Lys Glu Leu His Phe Cys Cys Thr Gly Cys  
 20 25 30  
 Ala Arg Val Tyr Ala Leu Leu Leu Asp Leu Asn Leu Glu Ser Phe Tyr  
 35 40 45  
 Asp Lys Leu Asn Asp Ser Thr Leu Ala Pro Val Thr Pro Gln Asp Ser  
 50 55 60  
 Met Ser Ala Leu Glu Leu Glu Gln Ala Leu Glu Glu Asn Asn Lys Gly  
 65 70 75 80  
 Asp Phe Ile Leu Asn Leu Leu Leu Glu Lys Thr His Cys Asn Ala Cys  
 85 90 95  
 Leu Trp Leu Asn Gln Lys Val Leu Glu Arg Leu Ser Gly Val Lys Lys  
 100 105 110  
 Val Ser Val Asn Phe Thr Thr His His Leu Gln Ile Val Phe Glu Lys  
 115 120 125  
 Ser Leu Asn Pro Lys Glu Ile Ile Gln Lys Ile Glu Ser Leu Gly Tyr  
 130 135 140  
 Gly Ala Lys Ile Tyr Asn Ala Gln Asn Tyr Thr Leu Lys Ala Gln Lys  
 145 150 155 160  
 Glu Gln Arg Ser Tyr Leu Leu Thr Leu Ser Val Gly Phe Phe Ala Thr  
 165 170 175  
 Met Asn Leu Met Phe Ile Ala Ile Ala Lys Tyr Ala Ser Tyr Gly Gly  
 180 185 190  
 Ala Ser Tyr Gly Gly Ala Asn Tyr Gly Ala Gly Met Asp Lys Leu Met  
 195 200 205  
 Gln Arg Asn Leu Asp Leu Val Ser Leu Phe Leu Ser Leu Leu Val Leu  
 210 215 220  
 Val Val Val Gly Arg Phe Phe Ile Lys Gly Ala Phe Tyr Gly Leu Lys  
 225 230 235 240  
 Asn Gly Val Leu Gly Met Asp Leu Ser Val Ser Phe Gly Ala Leu Ser  
 245 250 255  
 Ala Phe Val Tyr Ser Val Tyr Ala Met Leu Val Ser Gln Glu Thr Tyr  
 260 265 270  
 Phe Glu Ala Ser Ser Thr Ile Leu Thr Leu Val Phe Gly Ser Lys Phe

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275                      280                      285  
 Leu Glu Leu Lys Ala Arg Leu Phe Ala Asn Glu Lys Cys Leu Ala Leu  
     290                      295                      300  
 Glu Ser His Glu Ile His Ser Val Ile Val Val Glu Asn Gly Lys Gln  
     305                      310                      315                      320  
 Thr Glu Lys His Pro Lys Asp Val Ala Ile Gly Ser Val Val Trp Val  
                          325                      330                      335  
 Pro Ser Gly Ala Lys Ile Ala Leu Asp Gly Val Leu Leu Asn Asn Ala  
                          340                      345                      350  
 Ser Val Asp Ala Ser Leu Ile Ser Gly Glu Phe Lys Pro Leu Glu Leu  
                          355                      360                      365  
 Gly Val Asn Asp Pro Ile Leu Gly Gly Tyr Val Asn Val Gly Val Pro  
                          370                      375                      380  
 Phe Ser Tyr Gln Val Ser Ala Asn Phe Gln Asn Ser Arg Leu Ser Gly  
     385                      390                      395                      400  
 Leu Leu Glu Thr Leu Lys Lys Ser Phe Leu Glu Lys Pro Leu Ile Glu  
                          405                      410                      415  
 Ser Ser Ala Asn Gln Ile Ala Asp Ile Phe Ser Lys Ala Val Leu Phe  
                          420                      425                      430  
 Leu Ala Phe Val Ser Phe Leu Leu Trp Gln Phe Gly Leu Gly Gly Asn  
                          435                      440                      445  
 Phe Glu Lys Ala Leu Met Val Cys Ile Ser Val Leu Val Ile Ser Cys  
                          450                      455                      460  
 Pro Cys Ala Phe Ala Leu Ala Thr Pro Ile Ala Leu Val Ile Gly Val  
     465                      470                      475                      480  
 Phe Lys Asn Pro Leu Ile Val Phe Lys Glu Ala Leu Phe Leu Glu Thr  
                          485                      490                      495  
 Leu Ala Lys Val Lys Lys Ile Phe Ile Asp Lys Thr Gly Thr Leu Thr  
                          500                      505                      510  
 Gln Lys Glu Val Leu Leu Lys Glu Lys Ile Ile Tyr Glu Glu Phe Asp  
                          515                      520                      525  
 Gly Arg Leu Leu Lys Ser Leu Leu Lys Val Arg Glu His Leu Ala His  
                          530                      535                      540  
 Ser Ala Ile Leu Lys Ser Leu Asp Gly Asp Glu Val Ser Leu Glu Lys  
     545                      550                      555                      560  
 Ile Glu Phe Phe Ala His Gly Leu Lys Ala Ser Tyr Gln Asn Glu Thr  
                          565                      570                      575  
 Leu Leu Val Gly Ser Leu Lys Phe Leu Gly Ser Met Gly Val Asp Ile  
                          580                      585                      590

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Pro Met Lys Glu Ser Ala Asn Ile Met Val Gly Phe Ala Lys Asn Glu  
595 600 605

Thr Leu Cys Ala Leu Phe Ile Leu Glu Glu Arg Leu Lys Ala Asn Ala  
610 615 620

Lys Glu Val Val Gln Ala Leu Gln Asn Lys Gly Leu Glu Leu Glu Ile  
625 630 635 640

Leu Ser Gly Asp Asn Glu Ser Ser Val Lys Glu Cys Ala Lys Lys Leu  
645 650 655

Gly Ile Ser Asn Tyr His Ala His Leu Thr Pro Glu Asp Lys Ala Gln  
660 665 670

Thr Ile Ser Ser Tyr Lys Gly Val Cys Ala Met Val Gly Asp Gly Asn  
675 680 685

Asn Asp Ala Leu Ala Leu Lys Gln Ala Ser Val Ser Leu Gly Phe Glu  
690 695 700

Lys Ser Ala Leu Ser Lys Ser Ala Cys Asp Ile Leu Leu Leu Glu Glu  
705 710 715 720

Asp Leu Ser Leu Leu Lys Lys Ala Phe Asp Asn Ala Gln Lys Val Tyr  
725 730 735

Gln Val Val Leu Gln Asn Ile Val Leu Ser Leu Ile Tyr Asn Ala Ile  
740 745 750

Leu Ile Pro Val Ala Met Leu Gly Tyr Ile Asn Pro Leu Ile Ala Ser  
755 760 765

Leu Ser Met Ser Ala Ser Ser Leu Leu Val Val Leu Asn Ser Leu Arg  
770 775 780

Leu Lys Arg Ser \*

785

## (2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2751 Base pairs
  - (B) TYPE: Nucleotide
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear

- (vii) DIRECT SOURCE:
- (B) CLONE(S): HPS120

- (ix) FEATURES:
- (A) NAME/KEY: CDS
  - (B) POSITION: 1..2751

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

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ATT AAA AAA TTA ATT CTA TCC TCT CTT GTT TTC GCA TGT ATC AAT ACC Ile Lys Lys Leu Ile Leu Ser Ser Leu Val Phe Ala Cys Ile Asn Thr 790 795 800 805	48
AGC GTT GAA GCT TTA GAA AAT GAC GGC TCT AAA CCA AAC GAT TTG ACT Ser Val Glu Ala Leu Glu Asn Asp Gly Ser Lys Pro Asn Asp Leu Thr 810 815 820	96
TCT CCA AAA GAA GCC TCT CAA GAA TCT CAA AAA AAT GAA GCT CCA AAA Ser Pro Lys Glu Ala Ser Gln Glu Ser Gln Lys Asn Glu Ala Pro Lys 825 830 835	144
AAT GAA GTT CAA AGA AAT GAA GCT CAA AAA GAA ACC CCC CAA TCC AAT Asn Glu Val Gln Arg Asn Glu Ala Gln Lys Glu Thr Pro Gln Ser Asn 840 845 850	192
CAA ACG CCT AAA GAA ATG AAA GTC AAG TCC ATT TCT TAT GTC GGG CTT Gln Thr Pro Lys Glu Met Lys Val Lys Ser Ile Ser Tyr Val Gly Leu 855 860 865	240
TCT TAC ATG TCT GAC ATG CTC GCT AAT GAA ATT GTA AAG ATT CGT GTG Ser Tyr Met Ser Asp Met Leu Ala Asn Glu Ile Val Lys Ile Arg Val 870 875 880 885	288
GGC GAT ATT GTG GAT TCT AAA AAA ATA GAC ACC GCT GTT TTG GCT TTG Gly Asp Ile Val Asp Ser Lys Lys Ile Asp Thr Ala Val Leu Ala Leu 890 895 900	336
TTC AAT CAA GGG TAT TTT AAA GAC GTT TAT GCC ACT TTT GAA GGC GGC Phe Asn Gln Gly Tyr Phe Lys Asp Val Tyr Ala Thr Phe Glu Gly Gly 905 910 915	384
ATA TTA GAG TTT CAT TTT GAT GAA AAA GCC AGG ATT GCC GGG GTA GAA Ile Leu Glu Phe His Phe Asp Glu Lys Ala Arg Ile Ala Gly Val Glu 920 925 930	432
ATC AAG GGT TAT GGG ACT GAA AAG GAA AAA GAC GGC TTA AAA TCC CAA Ile Lys Gly Tyr Gly Thr Glu Lys Glu Lys Asp Gly Leu Lys Ser Gln 935 940 945	480
ATG GGG ATC AAA AAG GGC GAC ACC TTT GAT GAG CAA AAA TTA GAG CAT Met Gly Ile Lys Lys Gly Asp Thr Phe Asp Glu Gln Lys Leu Glu His 950 955 960 965	528
GCT AAA ACG GCT TTA AAA ACC GCT TTA GAG GGG CAG GGC TAT TAT GGG Ala Lys Thr Ala Leu Lys Thr Ala Leu Glu Gly Gln Gly Tyr Tyr Gly 970 975 980	576
AGC GTG GTG GAG GTG CGC ACA GAA AAG GTC AGT GAG GGT GCA TTA TTG Ser Val Val Glu Val Arg Thr Glu Lys Val Ser Glu Gly Ala Leu Leu 985 990 995	624
ATC GTG TTT GAT GTG AAT AGG GGG GAT AGC ATT TAT ATC AAA CAA TCC Ile Val Phe Asp Val Asn Arg Gly Asp Ser Ile Tyr Ile Lys Gln Ser 1000 1005 1010	672
ATT TAT GAG GGA AGC GCG AAA TTA AAA CGC CGC ATG ATT GAA TCT TTG Ile Tyr Glu Gly Ser Ala Lys Leu Lys Arg Arg Met Ile Glu Ser Leu 1015 1020 1025	720

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D



AGT GCG AAC AAG CAA CGA GAT TTC ATG GGC TGG ATG TGG GGC TTG AAT 768  
 Ser Ala Asn Lys Gln Arg Asp Phe Met Gly Trp Met Trp Gly Leu Asn  
 1030 1035 1040 1045

GAC GGG AAA TTG CGT TTA GAT CAA CTA GAA TAC GAT TCT ATG CGT ATC 816  
 Asp Gly Lys Leu Arg Leu Asp Gln Leu Glu Tyr Asp Ser Met Arg Ile  
 1050 1055 1060

CAA GAT GTG TAT ATG CGT AGG GGT TAC TTA GAC GCT CAT ATT TCT TCG 864  
 Gln Asp Val Tyr Met Arg Arg Gly Tyr Leu Asp Ala His Ile Ser Ser  
 1065 1070 1075

CCT TTT TTG AAA ACG GAT TTT TCT ACC CAT GAC GCT AAG CTT CAT TAT 912  
 Pro Phe Leu Lys Thr Asp Phe Ser Thr His Asp Ala Lys Leu His Tyr  
 1080 1085 1090

AAA GTC AAA GAG GGG ATC CAA TAC AGG ATT TCA GAC ATT TTA ATA GAG 960  
 Lys Val Lys Glu Gly Ile Gln Tyr Arg Ile Ser Asp Ile Leu Ile Glu  
 1095 1100 1105

ATT GAC AAC CCG GTA GTC CCC TTA AAA ACC TTA GAA AAA GCG CTT AAA 1008  
 Ile Asp Asn Pro Val Val Pro Leu Lys Thr Leu Glu Lys Ala Leu Lys  
 1110 1115 1120 1125

GTG AAA AGG AAA GAT GTC TTT AAT ATT GAG CAT TTA AGA GCG GAT GCG 1056  
 Val Lys Arg Lys Asp Val Phe Asn Ile Glu His Leu Arg Ala Asp Ala  
 1130 1135 1140

CAA ATT TTA AAA ACC GAA ATC GCC GAT AAG GGT TAT GCG TTT GCG GTG 1104  
 Gln Ile Leu Lys Thr Glu Ile Ala Asp Lys Gly Tyr Ala Phe Ala Val  
 1145 1150 1155

GTG AAG CCA GAC TTG GAT AAA GAT GAA AAA AAC GGG CTT GTG AAA GTC 1152  
 Val Lys Pro Asp Leu Asp Lys Asp Glu Lys Asn Gly Leu Val Lys Val  
 1160 1165 1170

ATT TAT CGT ATT GAA GTG GGC GAT ATG GTG TAT ATC AAT GAT GTC ATC 1200  
 Ile Tyr Arg Ile Glu Val Gly Asp Met Val Tyr Ile Asn Asp Val Ile  
 1175 1180 1185

ATT TCA GGG AAC CAG CGC ACG AGC GAT AGG ATC ATT AGA AGG GAG TTA 1248  
 Ile Ser Gly Asn Gln Arg Thr Ser Asp Arg Ile Ile Arg Arg Glu Leu  
 1190 1195 1200 1205

TTG TTA GGG CCT AAG GAT AAA TAC AAC TTG ACC AAA CTG AGA AAT TCC 1296  
 Leu Leu Gly Pro Lys Asp Lys Tyr Asn Leu Thr Lys Leu Arg Asn Ser  
 1210 1215 1220

GAA AAT TCT TTA AGG CGT TTA GGA TTC TTC TCT AAA GTC AAA ATT GAA 1344  
 Glu Asn Ser Leu Arg Arg Leu Gly Phe Phe Ser Lys Val Lys Ile Glu  
 1225 1230 1235

GAA AAA AGG GTT AAT AGC TCA CTC ATG GAT TTA TTA GTG AGC GTA GAA 1392  
 Glu Lys Arg Val Asn Ser Ser Leu Met Asp Leu Leu Val Ser Val Glu  
 1240 1245 1250

GAG GGG CGT ACT GGG CAG TTG CAA TTT GGG TTA GGC TAT GGC TCT TAT 1440  
 Glu Gly Arg Thr Gly Gln Leu Gln Phe Gly Leu Gly Tyr Gly Ser Tyr

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1255	1260	1265	
GGA GGG CTT ATG CTT AAT GGG AGC GTG AGC GAA AGA AAC CTT TTT GGC Gly Gly Leu Met Leu Asn Gly Ser Val Ser Glu Arg Asn Leu Phe Gly 1270 1275 1280 1285			1488
ACA GGG CAA AGC ATG AGC TTG TAT GCT AAC ATC GCT ACA GGG GGG GGT Thr Gly Gln Ser Met Ser Leu Tyr Ala Asn Ile Ala Thr Gly Gly Gly 1290 1295 1300			1536
AGA TCT TAT CCG GGC ATG CCA AAA GGA GCG GGG CGT ATG TTT GCC GGG Arg Ser Tyr Pro Gly Met Pro Lys Gly Ala Gly Arg Met Phe Ala Gly 1305 1310 1315			1584
AAT TTG AGC TTG ACT AAT CCA AGG ATT TTT GAC AGC TGG TAT AGC TCT Asn Leu Ser Leu Thr Asn Pro Arg Ile Phe Asp Ser Trp Tyr Ser Ser 1320 1325 1330			1632
ACG ATC AAC CTT TAT GCG GAT TAC AGG ATA AGC TAC CAA TAC ATC CAA Thr Ile Asn Leu Tyr Ala Asp Tyr Arg Ile Ser Tyr Gln Tyr Ile Gln 1335 1340 1345			1680
CAA GGC GGG GGC TTT GGG GTG AAT GTC GGG CGC ATG CTG GGT AAT AGA Gln Gly Gly Gly Phe Gly Val Asn Val Gly Arg Met Leu Gly Asn Arg 1350 1355 1360 1365			1728
ACC CAT GTG AGC TTA GGG TAT AAC TTG AAT GTT ACC AAA CTC CTT GGT Thr His Val Ser Leu Gly Tyr Asn Leu Asn Val Thr Lys Leu Leu Gly 1370 1375 1380			1776
TTC AGC AGC CCT TTA TAC AAC CGC TAC TAT TCC TCT GTT AAT GAA GTG Phe Ser Ser Pro Leu Tyr Asn Arg Tyr Tyr Ser Ser Val Asn Glu Val 1385 1390 1395			1824
GTT TCT CCA AGG CAA TGT TCT ACC CCC GCA TCG GTG ATT ATC AAT CGC Val Ser Pro Arg Gln Cys Ser Thr Pro Ala Ser Val Ile Ile Asn Arg 1400 1405 1410			1872
TTA TCA GGC GGT AAA ACC CCC TTA CAA CCT GAA AGC TGT TCT AGT CCT Leu Ser Gly Gly Lys Thr Pro Leu Gln Pro Glu Ser Cys Ser Ser Pro 1415 1420 1425			1920
GGA GCG ATC ACC ACT TCA CCA GAA ATA AGA GGT ATT TGG GAT AGG GAT Gly Ala Ile Thr Thr Ser Pro Glu Ile Arg Gly Ile Trp Asp Arg Asp 1430 1435 1440 1445			1968
TAC CAT ACG CCT ATC ACC AGC TCT TTC ACC CTT GAT GTG AGC TAT GAC Tyr His Thr Pro Ile Thr Ser Ser Phe Thr Leu Asp Val Ser Tyr Asp 1450 1455 1460			2016
AAC ACC GAT GAT TAT TAC TTC CCT AGA AAT GGG GTT ATC TTT AGT TCC Asn Thr Asp Asp Tyr Tyr Phe Pro Arg Asn Gly Val Ile Phe Ser Ser 1465 1470 1475			2064
TAT GCG ACG ATG TCT GGC TTG CCA AGC TCT GGC ACG CTC AAT TCT TGG Tyr Ala Thr Met Ser Gly Leu Pro Ser Ser Gly Thr Leu Asn Ser Trp 1480 1485 1490			2112
AAC GGG TTA GGC GGG AAT GTC CGT AAC ACC AAA GTT TAT GGT AAA TTC			2160

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Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly Lys Phe			
1495	1500	1505	
GCC GCT TAC CAC CAT TTG CAA AAA TAT TTA TTG ATA GAT TTG ATC GCT	2208		
Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu Ile Ala			
1510	1515	1520	1525
CGC TTT AAA ACG CAA GGA GGT TAT ATC TTT AGG TAT AAC ACC GAT GAT	2256		
Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr Asp Asp			
1530	1535	1540	
TAC TTG CCC TTA AAC TCC ACC TTC TAC ATG GGG GGC GTA ACC ACG GTG	2304		
Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr Thr Val			
1545	1550	1555	
AGA GGC TTT AGG AAC GGA TCG GTT ACT CCT AAA GAT GAG TTT GGC TTG	2352		
Arg Gly Phe Arg Asn Gly Ser Val Thr Pro Lys Asp Glu Phe Gly Leu			
1560	1565	1570	
TGG CTT GGA GGC GAT GGG ATT TTT ACC GCT TCT ACT GAA TTG AGC TAT	2400		
Trp Leu Gly Gly Asp Gly Ile Phe Thr Ala Ser Thr Glu Leu Ser Tyr			
1575	1580	1585	
GGG GTG CTA AAG GCG GCT AAA ATG CGC TTA GCG TGG TTT TTT GAC TTT	2448		
Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe Asp Phe			
1590	1595	1600	1605
GGT TTC TTA ACC TTT AAA ACC CCA ACT AGA GGG AGT TTT TTC TAT AAC	2496		
Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser Phe Phe Tyr Asn			
1610	1615	1620	
GCT CCT GTT ACG ACA GCG AAT TTT AAA GAT TAT GGC GTT ATA GGG GCT	2544		
Ala Pro Val Thr Thr Ala Asn Phe Lys Asp Tyr Gly Val Ile Gly Ala			
1625	1630	1635	
GGG TTT GAA AGA GCG ACT TGG AGG GCT TCC ACA GGC TTG CAG ATT GAA	2592		
Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly Leu Gln Ile Glu			
1640	1645	1650	
TGG ATT TCG CCC ATG GGG CCT TTG GTG TTG ATT TTC CCT ATA GCG TTT	2640		
Trp Ile Ser Pro Met Gly Pro Leu Val Leu Ile Phe Pro Ile Ala Phe			
1655	1660	1665	
TTC AAC CAA TGG GGC GAT GGC AAT GGC AAG AAA TGT AAA GGG CTA TGC	2688		
Phe Asn Gln Trp Gly Asp Gly Asn Gly Lys Lys Cys Lys Gly Leu Cys			
1670	1675	1680	1685
TTC AAC CCT AAC ATG GAC GAT TAC ACG CAA CAC TTT GAA TTT TCT ATG	2736		
Phe Asn Pro Asn Met Asp Asp Tyr Thr Gln His Phe Glu Phe Ser Met			
1690	1695	1700	
GGA ACA AGG TTT TAA	2751		
Gly Thr Arg Phe *			
1705			

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 917 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Ile Lys Lys Leu Ile Leu Ser Ser Leu Val Phe Ala Cys Ile Asn Thr  
 1 5 10 15  
 Ser Val Glu Ala Leu Glu Asn Asp Gly Ser Lys Pro Asn Asp Leu Thr  
 20 25 30  
 Ser Pro Lys Glu Ala Ser Gln Glu Ser Gln Lys Asn Glu Ala Pro Lys  
 35 40 45  
 Asn Glu Val Gln Arg Asn Glu Ala Gln Lys Glu Thr Pro Gln Ser Asn  
 50 55 60  
 Gln Thr Pro Lys Glu Met Lys Val Lys Ser Ile Ser Tyr Val Gly Leu  
 65 70 75 80  
 Ser Tyr Met Ser Asp Met Leu Ala Asn Glu Ile Val Lys Ile Arg Val  
 85 90 95  
 Gly Asp Ile Val Asp Ser Lys Lys Ile Asp Thr Ala Val Leu Ala Leu  
 100 105 110  
 Phe Asn Gln Gly Tyr Phe Lys Asp Val Tyr Ala Thr Phe Glu Gly Gly  
 115 120 125  
 Ile Leu Glu Phe His Phe Asp Glu Lys Ala Arg Ile Ala Gly Val Glu  
 130 135 140  
 Ile Lys Gly Tyr Gly Thr Glu Lys Glu Lys Asp Gly Leu Lys Ser Gln  
 145 150 155 160  
 Met Gly Ile Lys Lys Gly Asp Thr Phe Asp Glu Gln Lys Leu Glu His  
 165 170 175  
 Ala Lys Thr Ala Leu Lys Thr Ala Leu Glu Gly Gln Gly Tyr Tyr Gly  
 180 185 190  
 Ser Val Val Glu Val Arg Thr Glu Lys Val Ser Glu Gly Ala Leu Leu  
 195 200 205  
 Ile Val Phe Asp Val Asn Arg Gly Asp Ser Ile Tyr Ile Lys Gln Ser  
 210 215 220  
 Ile Tyr Glu Gly Ser Ala Lys Leu Lys Arg Arg Met Ile Glu Ser Leu  
 225 230 235 240  
 Ser Ala Asn Lys Gln Arg Asp Phe Met Gly Trp Met Trp Gly Leu Asn  
 245 250 255  
 Asp Gly Lys Leu Arg Leu Asp Gln Leu Glu Tyr Asp Ser Met Arg Ile  
 260 265 270  
 Gln Asp Val Tyr Met Arg Arg Gly Tyr Leu Asp Ala His Ile Ser Ser

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D

275                      280                      285  
 Pro Phe Leu Lys Thr Asp Phe Ser Thr His Asp Ala Lys Leu His Tyr  
 290                      295                      300  
 Lys Val Lys Glu Gly Ile Gln Tyr Arg Ile Ser Asp Ile Leu Ile Glu  
 305                      310                      315                      320  
 Ile Asp Asn Pro Val Val Pro Leu Lys Thr Leu Glu Lys Ala Leu Lys  
 325                      330                      335  
 Val Lys Arg Lys Asp Val Phe Asn Ile Glu His Leu Arg Ala Asp Ala  
 340                      345                      350  
 Gln Ile Leu Lys Thr Glu Ile Ala Asp Lys Gly Tyr Ala Phe Ala Val  
 355                      360                      365  
 Val Lys Pro Asp Leu Asp Lys Asp Glu Lys Asn Gly Leu Val Lys Val  
 370                      375                      380  
 Ile Tyr Arg Ile Glu Val Gly Asp Met Val Tyr Ile Asn Asp Val Ile  
 385                      390                      395                      400  
 Ile Ser Gly Asn Gln Arg Thr Ser Asp Arg Ile Ile Arg Arg Glu Leu  
 405                      410                      415  
 Leu Leu Gly Pro Lys Asp Lys Tyr Asn Leu Thr Lys Leu Arg Asn Ser  
 420                      425                      430  
 Glu Asn Ser Leu Arg Arg Leu Gly Phe Phe Ser Lys Val Lys Ile Glu  
 435                      440                      445  
 Glu Lys Arg Val Asn Ser Ser Leu Met Asp Leu Leu Val Ser Val Glu  
 450                      455                      460  
 Glu Gly Arg Thr Gly Gln Leu Gln Phe Gly Leu Gly Tyr Gly Ser Tyr  
 465                      470                      475                      480  
 Gly Gly Leu Met Leu Asn Gly Ser Val Ser Glu Arg Asn Leu Phe Gly  
 485                      490                      495  
 Thr Gly Gln Ser Met Ser Leu Tyr Ala Asn Ile Ala Thr Gly Gly Gly  
 500                      505                      510  
 Arg Ser Tyr Pro Gly Met Pro Lys Gly Ala Gly Arg Met Phe Ala Gly  
 515                      520                      525  
 Asn Leu Ser Leu Thr Asn Pro Arg Ile Phe Asp Ser Trp Tyr Ser Ser  
 530                      535                      540  
 Thr Ile Asn Leu Tyr Ala Asp Tyr Arg Ile Ser Tyr Gln Tyr Ile Gln  
 545                      550                      555                      560  
 Gln Gly Gly Gly Phe Gly Val Asn Val Gly Arg Met Leu Gly Asn Arg  
 565                      570                      575  
 Thr His Val Ser Leu Gly Tyr Asn Leu Asn Val Thr Lys Leu Leu Gly  
 580                      585                      590

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Phe Ser Ser Pro Leu Tyr Asn Arg Tyr Tyr Ser Ser Val Asn Glu Val  
 595 600 605  
 Val Ser Pro Arg Gln Cys Ser Thr Pro Ala Ser Val Ile Ile Asn Arg  
 610 615 620  
 Leu Ser Gly Gly Lys Thr Pro Leu Gln Pro Glu Ser Cys Ser Ser Pro  
 625 630 635 640  
 Gly Ala Ile Thr Thr Ser Pro Glu Ile Arg Gly Ile Trp Asp Arg Asp  
 645 650 655  
 Tyr His Thr Pro Ile Thr Ser Ser Phe Thr Leu Asp Val Ser Tyr Asp  
 660 665 670  
 Asn Thr Asp Asp Tyr Tyr Phe Pro Arg Asn Gly Val Ile Phe Ser Ser  
 675 680 685  
 Tyr Ala Thr Met Ser Gly Leu Pro Ser Ser Gly Thr Leu Asn Ser Trp  
 690 695 700  
 Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly Lys Phe  
 705 710 715 720  
 Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu Ile Ala  
 725 730 735  
 Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr Asp Asp  
 740 745 750  
 Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr Thr Val  
 755 760 765  
 Arg Gly Phe Arg Asn Gly Ser Val Thr Pro Lys Asp Glu Phe Gly Leu  
 770 775 780  
 Trp Leu Gly Gly Asp Gly Ile Phe Thr Ala Ser Thr Glu Leu Ser Tyr  
 785 790 795 800  
 Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe Asp Phe  
 805 810 815  
 Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser Phe Phe Tyr Asn  
 820 825 830  
 Ala Pro Val Thr Thr Ala Asn Phe Lys Asp Tyr Gly Val Ile Gly Ala  
 835 840 845  
 Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly Leu Gln Ile Glu  
 850 855 860  
 Trp Ile Ser Pro Met Gly Pro Leu Val Leu Ile Phe Pro Ile Ala Phe  
 865 870 875 880  
 Phe Asn Gln Trp Gly Asp Gly Asn Gly Lys Lys Cys Lys Gly Leu Cys  
 885 890 895  
 Phe Asn Pro Asn Met Asp Asp Tyr Thr Gln His Phe Glu Phe Ser Met  
 900 905 910

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D

Gly Thr Arg Phe \*  
915

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS130

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATG AAA AGA TTT GTT TTG TTT TTA TTG TTC ATG TGC GTT TGC GTT CAA	48
Met Lys Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln	
920 925 930	
GCT TAC GCC GAG CAA GAT TAC TTT TTT AGG GAT TTT AAA TCT AGA GAT	96
Ala Tyr Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp	
935 940 945	
TTG CCC CAA AAA CTC CAT CTT GAT AAA AAG CTC TCC CAA ACA ATA CAG	144
Leu Pro Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln	
950 955 960 965	
CCA TGC ATG CAA CTT AAC GCA TCA AAA CAC TAC ACT TCT ACC GGG GTT	192
Pro Cys Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val	
970 975 980	
AGA GAG CCT GAT AAA TGC ACA AAG AGT TTT AAA AAA TCC GCT CTC ATG	240
Arg Glu Pro Asp Lys Cys Thr Lys Ser Phe Lys Lys Ser Ala Leu Met	
985 990 995	
TCC TAT GAC TTA GCG CTA GGT TAT TTG GTG AGT AAG AAT AAG CAA TAC	288
Ser Tyr Asp Leu Ala Leu Gly Tyr Leu Val Ser Lys Asn Lys Gln Tyr	
1000 1005 1010	
GGC TTA AAG GCT ATA GAA ATT TTA AAC GCT TGG GCT AAA GAG CTT CAA	336
Gly Leu Lys Ala Ile Glu Ile Leu Asn Ala Trp Ala Lys Glu Leu Gln	
1015 1020 1025	
AGC GTG GAT ACT TAT CAG AGC GAG GAT AAT ATC AAT TTT TAC ATG CCT	384
Ser Val Asp Thr Tyr Gln Ser Glu Asp Asn Ile Asn Phe Tyr Met Pro	
1030 1035 1040 1045	
TAT ATG AAC ATG GCT TAT TGG TTT GTC AAA AAG GCG TTT CCT AGC CCA	432
Tyr Met Asn Met Ala Tyr Trp Phe Val Lys Lys Ala Phe Pro Ser Pro	
1050 1055 1060	

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GAA TAT GAA GAT TTC ATT AAG CGG ATG CGC CAG TAT TCT CAA TCA GCT 480  
 Glu Tyr Glu Asp Phe Ile Lys Arg Met Arg Gln Tyr Ser Gln Ser Ala  
 1065 1070 1075  
 CTT AAC ACT AAC CAT GGG GCG TGG GGC ATT CTT TTT GAT GTG AGT TCT 528  
 Leu Asn Thr Asn His Gly Ala Trp Gly Ile Leu Phe Asp Val Ser Ser  
 1080 1085 1090  
 GCG CTA GCG TTA GAC GAT AAT GCC CTT TTG CAC AAT AGC GCT AAT CGG 576  
 Ala Leu Ala Leu Asp Asp Asn Ala Leu Leu His Asn Ser Ala Asn Arg  
 1095 1100 1105  
 TGG CAG GAG TGG GTG TTT AAA GCC ATA GAT GAG AAT GGG GTT ATT GCT 624  
 Trp Gln Glu Trp Val Phe Lys Ala Ile Asp Glu Asn Gly Val Ile Ala  
 1110 1115 1120 1125  
 AGC GCG ATC ACT AGG AGC GAT ACG AGC GAT TAT CAT GGC GGC CCT ACA 672  
 Ser Ala Ile Thr Arg Ser Asp Thr Ser Asp Tyr His Gly Gly Pro Thr  
 1130 1135 1140  
 AAG GGC ATT AAG GGG ATA GCT TAT ACC AAT TTC GCG CTT CTT GCG CTA 720  
 Lys Gly Ile Lys Gly Ile Ala Tyr Thr Asn Phe Ala Leu Leu Ala Leu  
 1145 1150 1155  
 ACC ATA TCA GGC GAA TTG CTT TTT GAG AAC GGG TAT GAT TTG TGG GGT 768  
 Thr Ile Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly  
 1160 1165 1170  
 AGT GGA GCT GGG AAA AGG CTC TCT GTG GCG TAT AAC AAA GTT GCA ACA 816  
 Ser Gly Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr  
 1175 1180 1185  
 TGG ATT TTA AAC CCT GAA ACT TTC CCT TAT TTC CAG CCT AAC CTT ATC 864  
 Trp Ile Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile  
 1190 1195 1200 1205  
 GGG GTG CAT AAC AAC GCC TAT TTC ATT ATT TTA GCC AAG CAT TAT TCT 912  
 Gly Val His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser  
 1210 1215 1220  
 AGC CCT AGT GCA AAT GAG CTT TTA AAG CAA GGC GAT TTA CAC GAA GAT 960  
 Ser Pro Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp  
 1225 1230 1235  
 GGT TTC AGG CTG AAA CTC CGA TCG CCA TGA 990  
 Gly Phe Arg Leu Lys Leu Arg Ser Pro \*  
 1240 1245

## (2) INFORMATION FOR SEQ ID NO: 38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:



Met Lys Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln  
 1 5 10 15  
 Ala Tyr Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp  
 20 25 30  
 Leu Pro Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln  
 35 40 45  
 Pro Cys Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val  
 50 55 60  
 Arg Glu Pro Asp Lys Cys Thr Lys Ser Phe Lys Lys Ser Ala Leu Met  
 65 70 75 80  
 Ser Tyr Asp Leu Ala Leu Gly Tyr Leu Val Ser Lys Asn Lys Gln Tyr  
 85 90 95  
 Gly Leu Lys Ala Ile Glu Ile Leu Asn Ala Trp Ala Lys Glu Leu Gln  
 100 105 110  
 Ser Val Asp Thr Tyr Gln Ser Glu Asp Asn Ile Asn Phe Tyr Met Pro  
 115 120 125  
 Tyr Met Asn Met Ala Tyr Trp Phe Val Lys Lys Ala Phe Pro Ser Pro  
 130 135 140  
 Glu Tyr Glu Asp Phe Ile Lys Arg Met Arg Gln Tyr Ser Gln Ser Ala  
 145 150 155 160  
 Leu Asn Thr Asn His Gly Ala Trp Gly Ile Leu Phe Asp Val Ser Ser  
 165 170 175  
 Ala Leu Ala Leu Asp Asp Asn Ala Leu Leu His Asn Ser Ala Asn Arg  
 180 185 190  
 Trp Gln Glu Trp Val Phe Lys Ala Ile Asp Glu Asn Gly Val Ile Ala  
 195 200 205  
 Ser Ala Ile Thr Arg Ser Asp Thr Ser Asp Tyr His Gly Gly Pro Thr  
 210 215 220  
 Lys Gly Ile Lys Gly Ile Ala Tyr Thr Asn Phe Ala Leu Leu Ala Leu  
 225 230 235 240  
 Thr Ile Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly  
 245 250 255  
 Ser Gly Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr  
 260 265 270  
 Trp Ile Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile  
 275 280 285  
 Gly Val His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser  
 290 295 300  
 Ser Pro Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp

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(2) INFORMATION FOR SEO ID NO: 39:

(A) LENGTH: 1482 Base pairs  
(B) TYPE: Nucleotide  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(B) CLONE(S) : HPS133

(A) NAME/KEY: CDS  
(B) POSITION:1..1482

ATG	CAA	AGT	CTT	AGT	TGG	CTG	AAT	TTA	GCG	TTT	CGT	TGG	CTC	TTT	ATA	48
Met	Gln	Ser	Leu	Ser	Trp	Leu	Asn	Leu	Ala	Phe	Arg	Trp	Leu	Phe	Ile	
				335					340					345		
ACA	GGG	CTT	GGC	TAT	TAT	ATA	ATG	ACT	TTA	TTG	CAA	TGG	TAT	CAT	TAC	96
Thr	Gly	Leu	Gly	Tyr	Tyr	Ile	Met	Thr	Leu	Leu	Gln	Trp	Tyr	His	Tyr	
			350					355					360			
AGC	GTG	TTT	AGG	ATC	TTA	ACC	AAG	CAC	CAC	AAA	ATG	CGT	TGG	CAT	GGG	144
Ser	Val	Phe	Arg	Ile	Leu	Thr	Lys	His	His	Lys	Met	Arg	Trp	His	Gly	
		365					370					375				
ATT	TAT	TTT	TTA	TTG	CCT	TTA	GGG	GTG	TTT	ATT	CTG	TCG	TAT	GCT	TTC	192
Ile	Tyr	Phe	Leu	Leu	Pro	Leu	Gly	Val	Phe	Ile	Leu	Ser	Tyr	Ala	Phe	
	380					385					390					
ACA	ATG	CCG	TTT	GTT	TTT	GAT	TTC	TTT	TGC	GCG	GTT	ATT	CAA	ATG	CCC	240
Thr	Met	Pro	Phe	Val	Phe	Asp	Phe	Phe	Cys	Gly	Val	Ile	Gln	Met	Pro	
395					400					405					410	
ATG	CTC	ATT	GTT	TGG	GCC	AAA	CGC	AAC	GAC	AAG	CCT	TTA	GTT	TTC	ACG	288
Met	Leu	Ile	Val	Trp	Ala	Lys	Arg	Asn	Asp	Lys	Pro	Leu	Val	Phe	Thr	
				415					420					425		
CCA	AGG	GTG	AAG	CGC	TTT	TTT	ATC	TTC	TTA	TTA	TTA	TTT	TTA	ATC	TTG	336
Pro	Arg	Val	Lys	Arg	Phe	Phe	Ile	Phe	Leu	Leu	Leu	Phe	Leu	Ile	Leu	
			430					435					440			
CAT	GAA	ATC	TTA	AAT	ATA	GAA	TTA	GTC	CCT	TTG	GAT	GGG	ATT	TCG	CTC	384
His	Glu	Ile	Leu	Asn	Ile	Glu	Leu	Val	Pro	Leu	Asp	Gly	Ile	Ser	Leu	
		445					450					455				
GCG	CTA	GGC	TAT	TTG	TGT	TTG	TTT	ATA	TTC	GTT	TTA	AGC	GCT	TCT	TTA	432
Ala	Leu	Gly	Tyr	Leu	Cys	Leu	Phe	Ile	Phe	Val	Leu	Ser	Ala	Ser	Leu	

460	465	470	
ATC TCT GAA AAA GCC TTA TCC AAG CAG TAT TTG CAA ACC GCT AAA GAT Ile Ser Glu Lys Ala Leu Ser Lys Gln Tyr Leu Gln Thr Ala Lys Asp 475 480 485 490			480
AAA ATC ACC TCT TTA AAG AAT TTA AAA GTC ATC GCC ATT ACC GGA AGC Lys Ile Thr Ser Leu Lys Asn Leu Lys Val Ile Ala Ile Thr Gly Ser 495 500 505			528
TTT GGG AAA ACC AGC ACC AAA AAT TTC TTG CTT CAA ATC TTA CAA ACC Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu Leu Gln Ile Leu Gln Thr 510 515 520			576
ACA TTC AAC GCG CAT GCA AGC CCC AAA AGC GTC AAT ACC CTT TTA GGG Thr Phe Asn Ala His Ala Ser Pro Lys Ser Val Asn Thr Leu Leu Gly 525 530 535			624
CTT GCG AAT GAT ATT AAT CAG AAT TTA GAC GAT AGG AGT GAA ATC TAT Leu Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp Arg Ser Glu Ile Tyr 540 545 550			672
ATC GCT GAA GCC GGG GCA AGG AAT AAG GGC GAT ATT AAA GAA ATC ACC Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp Ile Lys Glu Ile Thr 555 560 565 570			720
TGT CTC ATT GAA CCG CAC CTT GTT GTG GTT GCA GAA GTG GGC GAA CAG Cys Leu Ile Glu Pro His Leu Val Val Ala Glu Val Gly Glu Gln 575 580 585			768
CAT TTA GAA TAC TTT AAA ACT TTA GAA AAT ATT TGC GAG ACT AAA GCG His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile Cys Glu Thr Lys Ala 590 595 600			816
GAA TTA TTG GAT TCC AAA CGC TTA GAA AAA GCC TTT TGT TAC TCG GTG Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala Phe Cys Tyr Ser Val 605 610 615			864
GAA AAG ATC AAG CCC TAT GCC CCT AAA GAT AGC CCT TTA ATA GAC TAT Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu Ile Asp Tyr 620 625 630			912
TCT AGC CTG GTT AAA AAC ATC CAA TCC ACT TTA AAA GGC ACT TCT TTT Ser Ser Leu Val Lys Asn Ile Gln Ser Thr Leu Lys Gly Thr Ser Phe 635 640 645 650			960
GAA ATG CTT ATA GGT AGC GTT TGG GAA AGA TTT GAA ACA AAG GTT CTA Glu Met Leu Ile Gly Ser Val Trp Glu Arg Phe Glu Thr Lys Val Leu 655 660 665			1008
GGG GAG TTT AGC GCT TAT AAT ATC GCT TCA GCC ATT TTA ATC GCT AAG Gly Glu Phe Ser Ala Tyr Asn Ile Ala Ser Ala Ile Leu Ile Ala Lys 670 675 680			1056
CAT TTA GGC TTA GAG ACC GAA AGG ATC AAA CGG CTT GTT TTA GAA CTC His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val Leu Glu Leu 685 690 695			1104
AAC CCT ATT GCT CAT CGT TTG CAA CTT TTG GAA GTG AAT CAA AAA ATC			1152

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Asn Pro Ile Ala His Arg Leu Gln Leu Leu Glu Val Asn Gln Lys Ile  
700 705 710

ATC ATA GAC GAT AGC TTT AAT GGG AAT TTA AAG GGC ATG TTA GAG GGC 1200  
Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met Leu Glu Gly  
715 720 725 730

ATT CGT TTA GCG AGT TTG CAC AAA GGG CGT AAA GTC ATT GTA ACA CCG 1248  
Ile Arg Leu Ala Ser Leu His Lys Gly Arg Lys Val Ile Val Thr Pro  
735 740 745

GGC TTA GTG GAA AGC AAT ACA GAA AGT AAT GAG GCT TTA GCG CAA AAA 1296  
Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu Ala Gln Lys  
750 755 760

ATA GAC GGG GTT TTT GAT GTC GCT ATC ATC ACA GGG GAG TTG AAT TCC 1344  
Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu Leu Asn Ser  
765 770 775

AAA ACG ATT GCT TCA CAA TTG AAA ACC CCC CAA AAA ATC TTA CTC AAG 1392  
Lys Thr Ile Ala Ser Gln Leu Lys Thr Pro Gln Lys Ile Leu Leu Lys  
780 785 790

GAT AAG GCG CAA TTG GAA AAT ATC TTA CAA GCC ACC ACG ATT CAA GGC 1440  
Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr Ile Gln Gly  
795 800 805 810

GAT TTG ATT TTA TTC GCT AAT GAC GCC CCT AAT TAC ATT TAG 1482  
Asp Leu Ile Leu Phe Ala Asn Asp Ala Pro Asn Tyr Ile \*  
815 820

## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met Gln Ser Leu Ser Trp Leu Asn Leu Ala Phe Arg Trp Leu Phe Ile  
1 5 10 15

Thr Gly Leu Gly Tyr Tyr Ile Met Thr Leu Leu Gln Trp Tyr His Tyr  
20 25 30

Ser Val Phe Arg Ile Leu Thr Lys His His Lys Met Arg Trp His Gly  
35 40 45

Ile Tyr Phe Leu Leu Pro Leu Gly Val Phe Ile Leu Ser Tyr Ala Phe  
50 55 60

Thr Met Pro Phe Val Phe Asp Phe Phe Cys Gly Val Ile Gln Met Pro  
65 70 75 80

Met Leu Ile Val Trp Ala Lys Arg Asn Asp Lys Pro Leu Val Phe Thr  
85 90 95

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Pro Arg Val Lys Arg Phe Phe Ile Phe Leu Leu Leu Phe Leu Ile Leu  
 100 105 110  
 His Glu Ile Leu Asn Ile Glu Leu Val Pro Leu Asp Gly Ile Ser Leu  
 115 120 125  
 Ala Leu Gly Tyr Leu Cys Leu Phe Ile Phe Val Leu Ser Ala Ser Leu  
 130 135 140  
 Ile Ser Glu Lys Ala Leu Ser Lys Gln Tyr Leu Gln Thr Ala Lys Asp  
 145 150 155 160  
 Lys Ile Thr Ser Leu Lys Asn Leu Lys Val Ile Ala Ile Thr Gly Ser  
 165 170 175  
 Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu Leu Gln Ile Leu Gln Thr  
 180 185 190  
 Thr Phe Asn Ala His Ala Ser Pro Lys Ser Val Asn Thr Leu Leu Gly  
 195 200 205  
 Leu Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp Arg Ser Glu Ile Tyr  
 210 215 220  
 Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp Ile Lys Glu Ile Thr  
 225 230 235 240  
 Cys Leu Ile Glu Pro His Leu Val Val Val Ala Glu Val Gly Glu Gln  
 245 250 255  
 His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile Cys Glu Thr Lys Ala  
 260 265 270  
 Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala Phe Cys Tyr Ser Val  
 275 280 285  
 Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu Ile Asp Tyr  
 290 295 300  
 Ser Ser Leu Val Lys Asn Ile Gln Ser Thr Leu Lys Gly Thr Ser Phe  
 305 310 315 320  
 Glu Met Leu Ile Gly Ser Val Trp Glu Arg Phe Glu Thr Lys Val Leu  
 325 330 335  
 Gly Glu Phe Ser Ala Tyr Asn Ile Ala Ser Ala Ile Leu Ile Ala Lys  
 340 345 350  
 His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val Leu Glu Leu  
 355 360 365  
 Asn Pro Ile Ala His Arg Leu Gln Leu Leu Glu Val Asn Gln Lys Ile  
 370 375 380  
 Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met Leu Glu Gly  
 385 390 395 400  
 Ile Arg Leu Ala Ser Leu His Lys Gly Arg Lys Val Ile Val Thr Pro

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405 410 415

Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu Ala Gln Lys  
420 425 430

Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu Leu Asn Ser  
435 440 445

Lys Thr Ile Ala Ser Gln Leu Lys Thr Pro Gln Lys Ile Leu Leu Lys  
450 455 460

Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr Ile Gln Gly  
465 470 475 480

Asp Leu Ile Leu Phe Ala Asn Asp Ala Pro Asn Tyr Ile \*

485 490

## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPC134

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..600

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG TCA AGC GCT CTG TTA GGC TTA CAA ATT GTT TTA GCG GTA TTG ATT 48  
Met Ser Ser Ala Leu Leu Gly Leu Gln Ile Val Leu Ala Val Leu Ile  
495 500 505 510

GTG GTG GTG GTT TTG TTG CAA AAA AGT TCT AGC ATC GGC TTA GGG ACT 96  
Val Val Val Val Leu Leu Gln Lys Ser Ser Ser Ile Gly Leu Gly Thr  
515 520 525

TAT AGC GGG AGT AAT GAG TCT TTA TTT GGC GCT AAA GGG CCC GCG TGC 144  
Tyr Ser Gly Ser Asn Glu Ser Leu Phe Gly Ala Lys Gly Pro Ala Cys  
530 535 540

TTT ATG GCG AAA TTG ACC ATG TTT TTA GGG CTG TTA TTT GTT ATC AAC 192  
Phe Met Ala Lys Leu Thr Met Phe Leu Gly Leu Leu Phe Val Ile Asn  
545 550 555

ACC ATC GCT TTG GGC TAT TTT TAC AAC AAA GAA TAC GGC AAA AGC ATT 240  
Thr Ile Ala Leu Gly Tyr Phe Tyr Asn Lys Glu Tyr Gly Lys Ser Ile  
560 565 570

TTA GAT GAA ACT AAA ACC AAC AAA GAG CTT TCG CCC TTA GTC CCT GCC 288  
Leu Asp Glu Thr Lys Thr Asn Lys Glu Leu Ser Pro Leu Val Pro Ala

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(2) INFORMATION FOR SEQ ID NO: 42:

(A) LENGTH: 200 Amino acids

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met	Ser	Ser	Ala	Leu	Leu	Gly	Leu	Gln	Ile	Val	Leu	Ala	Val	Leu	Ile
1				5					10					15	
Val	Val	Val	Val	Leu	Leu	Gln	Lys	Ser	Ser	Ser	Ile	Gly	Leu	Gly	Thr
			20					25					30		
Tyr	Ser	Gly	Ser	Asn	Glu	Ser	Leu	Phe	Gly	Ala	Lys	Gly	Pro	Ala	Cys
		35					40					45			
Phe	Met	Ala	Lys	Leu	Thr	Met	Phe	Leu	Gly	Leu	Leu	Phe	Val	Ile	Asn
	50					55					60				
Thr	Ile	Ala	Leu	Gly	Tyr	Phe	Tyr	Asn	Lys	Glu	Tyr	Gly	Lys	Ser	Ile
65					70					75					80
Leu	Asp	Glu	Thr	Lys	Thr	Asn	Lys	Glu	Leu	Ser	Pro	Leu	Val	Pro	Ala
				85					90					95	

Thr Gly Thr Leu Asn Pro Thr Leu Asn Pro Thr Leu Asn Pro Thr Leu  
 100 105 110

Asn Pro Leu Glu Gln Ala Pro Thr Asn Pro Leu Met Pro Lys Gln Thr  
 115 120 125

Pro Asn Glu Leu Pro Lys Glu Pro Ala Lys Ala Pro Ser Val Glu Ser  
 130 135 140

Pro Lys Gln Asn Glu Lys Asn Glu Lys Asn Asp Ala Lys Glu Asn Gly  
 145 150 155 160

Ile Lys Gly Val Glu Lys Thr Lys Glu Asn Ala Lys Thr Pro Pro Thr  
 165 170 175

Thr His Gln Lys Pro Lys Thr His Ala Thr Gln Thr Asn Ala His Thr  
 180 185 190

Asn Gln Lys Lys Asp Glu Lys \*  
 195 200

## (2) INFORMATION FOR SEQ ID NO: 43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1536 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS143

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1536

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG AAA AAA CTT CTT TAT ACC ATA CTC GCG CTT CTT TTA ATC GGC CTT	48
Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile Gly Leu	
205 210 215	
TTA ACA ATC TAT CTC ATC CTT TTT ACA GAA TGG GGG AAT AAG ATC ATC	96
Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys Ile Ile	
220 225 230	
GCT TCG TAT ATA GAG AAA AAA ATC AAC CCG AAC GAG CAC TAC TTG AGC	144
Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr Leu Ser	
235 240 245	
GTT AAA ACC TTT AAA TTG AGA TTC AAC TCT TTG GAT TTT AAA GCT CAA	192
Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys Ala Gln	
250 255 260	
GCC AAC GAT GAT TCC ACG CTC ATT CTT AAG GGG GAT TTT TCA CTT TTA	240
Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly Asp Phe Ser Leu Leu	

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265		270		275		280	
AAG CAA AGC GTA AAT TTG AAT TAC CAT ATA GAT ATT AAA GAT TTA CGC							288
Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp Ile Lys Asp Leu Arg							
	285			290		295	
TCT TTC AAA GAA TGG ATA CCC TAC CCT TTA AGG GGG GCT GTT ATC ACT							336
Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg Gly Ala Val Ile Thr							
	300			305		310	
TCT GGG AAT ATT AAA GGG CAT AGA AAA GCC CTT ATG ATT CAA GGC GTC							384
Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu Met Ile Gln Gly Val							
	315			320		325	
TCT AAT GTG GCT CAA TCC CAC ACT GCC TAC AAT GCC CTT TTA GAT GAT							432
Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn Ala Leu Leu Asp Asp							
	330			335		340	
TTC AAG CTT TCT CGC TTA AAT TTG AAC GCA CAA GAC GCC AAT TTA GAA							480
Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln Asp Ala Asn Leu Glu							
	345			350		355	360
GAT TTG CTT TAT TTA ATC AAT CGC CCC GCT TAT GCG AAC GCA AAA GTG							528
Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr Ala Asn Ala Lys Val							
		365		370		375	
TCC TTA CAG GCG GAT TTT AAC TCT CTA AAG CCT TTA GAG GGG CAT TTG							576
Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro Leu Glu Gly His Leu							
	380			385		390	
ATC CTA ACA GCT AAT AAC GCT TTA ATC AAT AAC GCC CTA ATC AAT CAA							624
Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn Ala Leu Ile Asn Gln							
	395			400		405	
ATT TTT CAT TTA AAC CTT AAA GAC ACG CTT GTT TTC AGC CTC TCG CAT							672
Ile Phe His Leu Asn Leu Lys Asp Thr Leu Val Phe Ser Leu Ser His							
	410			415		420	
TCA AGC GAC TTT AAA GGA AAC AAA GCC ATC AGC GAT ACC ACC CTG ACT							720
Ser Ser Asp Phe Lys Gly Asn Lys Ala Ile Ser Asp Thr Thr Leu Thr							
	425			430		435	440
AGC CCT TTA GCC AAT TTC AAA GCC CTA AAA AGC GAA TAC CTT TTC TCT							768
Ser Pro Leu Ala Asn Phe Lys Ala Leu Lys Ser Glu Tyr Leu Phe Ser							
	445			450		455	
ATT TTA AAA CTC AAC GCC CCC TAC ACT TTA GAA ATC CCC AAT CTA GCC							816
Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu Ile Pro Asn Leu Ala							
	460			465		470	
AAA CTC TAT AAC ATT ACC AAC CAC CCC TTA AAA GGG AGC TTG ACT TTA							864
Lys Leu Tyr Asn Ile Thr Asn His Pro Leu Lys Gly Ser Leu Thr Leu							
	475			480		485	
AAA GGC GCT ATA GAA CAA AGC CCC AAA CTT TTA AAA GTC AGC GGC CAT							912
Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu Lys Val Ser Gly His							
	490			495		500	
TCA AAT TTA CTA GAC GGC GCG CTG GAT TTC ACG CTT TTA AAT AAA GAT							960

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Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr Leu Leu Asn Lys Asp  
 505 510 515 520

TTG AAA GGG CGT TTT TCC AAT ATT TCC ACT TTA AAA GCT TTA GAT TTA 1008  
 Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu Lys Ala Leu Asp Leu  
 525 530 535

TTC CAT TAC CCT AAG TTT TTC CAA TCC GTT GCA GAC GCT AAT TTG GAT 1056  
 Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala Asp Ala Asn Leu Asp  
 540 545 550

TAT GAT CTT ATC GCT AAG CAA GGC GTA TTG AAA GCC CGC CTA AAA AAC 1104  
 Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys Ala Arg Leu Lys Asn  
 555 560 565

GCA AGA TTC CTC AAA AAT GCA TTC AGC GAT TTT CTC TAC TCC ATT TCT 1152  
 Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser Ile Ser  
 570 575 580

AAA TTT GAT ATT ACA AAA GAA ATT TAT AAC GAT GCC AAT CTG GTA AGC 1200  
 Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp Ala Asn Leu Val Ser  
 585 590 595 600

CAA ATC AAC CAG CAA CGC CTG CTC TCT GAT CTG AGT TTA AAA AGC CCC 1248  
 Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu Ser Leu Lys Ser Pro  
 605 610 615

AAA ACC CAA TTG AAA ATC CAT AAC GGT TTG TTG GAT TTA AAC ACC AAA 1296  
 Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu Asp Leu Asn Thr Lys  
 620 625 630

CAA ATG AAC ATG CTC ATG GAT GCG GAA ATT TTA AAA TTC ATT TTT AAA 1344  
 Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu Lys Phe Ile Phe Lys  
 635 640 645

ATG AAA CTT CAA GGC AAC ATG CAC CAG CCA AAA TTT TCT CTC ATT TTA 1392  
 Met Lys Leu Gln Gly Asn Met His Gln Pro Lys Phe Ser Leu Ile Leu  
 650 655 660

AAC GAA AAA GCC ATT CAG CAA AAC TTG CAA CAA GGC TTG AAA GAA ATC 1440  
 Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys Glu Ile  
 665 670 675 680

TTA AAA AAC GAC ACC CTT AAA AAA GGT TTA GAT CAT TTG CTT AAA GAT 1488  
 Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu Lys Asp  
 685 690 695

GAT AAG CTC AAA GAA AAG CTT GAA AAA GGG CTT AAG GGG CTT TTT TAA 1536  
 Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu Phe \*  
 700 705 710

## (2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 Amino acids
  - (B) TYPE: Amino acid
  - (D) TOPOLOGY: linear

00980116-113001

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile Gly Leu  
 1 5 10 15  
 Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys Ile Ile  
 20 25 30  
 Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr Leu Ser  
 35 40 45  
 Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys Ala Gln  
 50 55 60  
 Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly Asp Phe Ser Leu Leu  
 65 70 75 80  
 Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp Ile Lys Asp Leu Arg  
 85 90 95  
 Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg Gly Ala Val Ile Thr  
 100 105 110  
 Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu Met Ile Gln Gly Val  
 115 120 125  
 Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn Ala Leu Leu Asp Asp  
 130 135 140  
 Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln Asp Ala Asn Leu Glu  
 145 150 155 160  
 Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr Ala Asn Ala Lys Val  
 165 170 175  
 Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro Leu Glu Gly His Leu  
 180 185 190  
 Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn Ala Leu Ile Asn Gln  
 195 200 205  
 Ile Phe His Leu Asn Leu Lys Asp Thr Leu Val Phe Ser Leu Ser His  
 210 215 220  
 Ser Ser Asp Phe Lys Gly Asn Lys Ala Ile Ser Asp Thr Thr Leu Thr  
 225 230 235 240  
 Ser Pro Leu Ala Asn Phe Lys Ala Leu Lys Ser Glu Tyr Leu Phe Ser  
 245 250 255  
 Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu Ile Pro Asn Leu Ala  
 260 265 270  
 Lys Leu Tyr Asn Ile Thr Asn His Pro Leu Lys Gly Ser Leu Thr Leu  
 275 280 285  
 Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu Lys Val Ser Gly His  
 290 295 300

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Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr Leu Leu Asn Lys Asp  
 305 310 315 320  
 Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu Lys Ala Leu Asp Leu  
 325 330 335  
 Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala Asp Ala Asn Leu Asp  
 340 345 350  
 Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys Ala Arg Leu Lys Asn  
 355 360 365  
 Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser Ile Ser  
 370 375 380  
 Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp Ala Asn Leu Val Ser  
 385 390 395 400  
 Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu Ser Leu Lys Ser Pro  
 405 410 415  
 Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu Asp Leu Asn Thr Lys  
 420 425 430  
 Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu Lys Phe Ile Phe Lys  
 435 440 445  
 Met Lys Leu Gln Gly Asn Met His Gln Pro Lys Phe Ser Leu Ile Leu  
 450 455 460  
 Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys Glu Ile  
 465 470 475 480  
 Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu Lys Asp  
 485 490 495  
 Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu Phe \*  
 500 505 510

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS144

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..540

00000115 113001

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG AAG AGA TCT TCT GTA TTT AGT TTC TTG GTA GCT TTT TTA TTG GTA 48  
 Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val  
 515 520 525

GCT GGC TGT AGT CAT AAA ATG GAT AAT AAG ACT GTG GCC GGC GAT GTG 96  
 Ala Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val  
 530 535 540

AGT GCT AAA ACG GTT CAG ACT GCA CCT GTT ACT ACA GAA CCA GCT CCA 144  
 Ser Ala Lys Thr Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro  
 545 550 555 560

GAG AAA GAA GAG CCT AAA CAA GAG CCA GCT CCA GTG GTT GAA GAA AAA 192  
 Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys  
 565 570 575

CCG GCT GTT GAG AGC GGG ACT ATC ATC GCT TCT ATT TAT TTT GAT TTT 240  
 Pro Ala Val Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe  
 580 585 590

GAC AAG TAT GAA ATC AAA GAA TCC GAT CAA GAG ACT TTA GAT GAG ATC 288  
 Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile  
 595 600 605

GTG CAA AAA GCT AAA GAA AAC CAC ATG CAA GTG CTT TTG GAA GGC AAT 336  
 Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn  
 610 615 620

ACC GAT GAA TTT GGC TCT AGC GAA TAC AAC CAA GCG CTT GGC GTT AAA 384  
 Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys  
 625 630 635 640

AGG ACT TTG AGC GTG AAA AAC GCT TTA GTC ATT AAA GGG GTA GAA AAA 432  
 Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys  
 645 650 655

GAT ATG ATC AAA ACC ATC AGT TTT GGT GAA ACC AAA CCC AAA TGC GCC 480  
 Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Thr Lys Pro Lys Cys Ala  
 660 665 670

CAA AAA ACT AGA GAG TGT TAT AAA GAA AAC AGA AGA GTG GAT GTC AAA 528  
 Gln Lys Thr Arg Glu Cys Tyr Lys Glu Asn Arg Arg Val Asp Val Lys  
 675 680 685

TTA ATG AAG TAA 540  
 Leu Met Lys \*  
 690

## (2) INFORMATION FOR SEQ ID NO: 46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val  
 1 5 10 15  
 Ala Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val  
 20 25 30  
 Ser Ala Lys Thr Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro  
 35 40 45  
 Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys  
 50 55 60  
 Pro Ala Val Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe  
 65 70 75 80  
 Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile  
 85 90 95  
 Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn  
 100 105 110  
 Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys  
 115 120 125  
 Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys  
 130 135 140  
 Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Thr Lys Pro Lys Cys Ala  
 145 150 155 160  
 Gln Lys Thr Arg Glu Cys Tyr Lys Glu Asn Arg Arg Val Asp Val Lys  
 165 170 175  
 Leu Met Lys \*  
 180

## (2) INFORMATION FOR SEQ ID NO: 47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPC140, HPC150, HPC179

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1560

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CAA ATG ATA AAA AAG AAT AGA ACG CTG TTT CTT AGT CTA GCC CTT TGC

Gln Met Ile Lys Lys Asn Arg Thr Leu Phe Leu Ser Leu Ala Leu Cys	
185 190 195	
GCT AGC ATA AGT TAT GCC GAA GAT GAT GGA GGG TTT TTC ACC GTC GGT	96
Ala Ser Ile Ser Tyr Ala Glu Asp Asp Gly Gly Phe Phe Thr Val Gly	
200 205 210	
TAT CAG CTC GGG CAA GTC ATG CAA GAT GTC CAA AAC CCA GGC GGC GCT	144
Tyr Gln Leu Gly Gln Val Met Gln Asp Val Gln Asn Pro Gly Gly Ala	
215 220 225	
AAA AGC GAC GAA CTC GCC AGA GAG CTT AAC GCT GAT GTA ACG AAC AAC	192
Lys Ser Asp Glu Leu Ala Arg Glu Leu Asn Ala Asp Val Thr Asn Asn	
230 235 240	
ATT TTA AAC AAC AAC ACC GGA GGC AAC ATC GCA GGG GCG TTG AGT AAC	240
Ile Leu Asn Asn Asn Thr Gly Gly Asn Ile Ala Gly Ala Leu Ser Asn	
245 250 255 260	
GCT TTC TCC CAA TAC CTT TAT TCG CTT TTA GGG GCT TAC CCC ACA AAA	288
Ala Phe Ser Gln Tyr Leu Tyr Ser Leu Leu Gly Ala Tyr Pro Thr Lys	
265 270 275	
CTC AAT GGT AGC GAT GTG TCT GCG AAC GCT CTT TTA AGT GGT GCG GTA	336
Leu Asn Gly Ser Asp Val Ser Ala Asn Ala Leu Leu Ser Gly Ala Val	
280 285 290	
GGC TCT GGG ACT TGT GCG GCT GCA GGG ACG GCT GGT GGC ACT TCT CTT	384
Gly Ser Gly Thr Cys Ala Ala Ala Gly Thr Ala Gly Gly Thr Ser Leu	
295 300 305	
AAC ACT CAA AGC ACT TGC ACC GTT GCG GGC TAT TAC TGG CTC CCT AGC	432
Asn Thr Gln Ser Thr Cys Thr Val Ala Gly Tyr Tyr Trp Leu Pro Ser	
310 315 320	
TTG ACT GAC AGG ATT TTA AGC ACG ATC GGC AGC CAG ACT AAC TAC GGC	480
Leu Thr Asp Arg Ile Leu Ser Thr Ile Gly Ser Gln Thr Asn Tyr Gly	
325 330 335 340	
ACG AAC ACC AAT TTC CCC AAC ATG CAA CAA CAG CTC ACC TAC TTG AAT	528
Thr Asn Thr Asn Phe Pro Asn Met Gln Gln Gln Leu Thr Tyr Leu Asn	
345 350 355	
GCG GGG AAT GTG TTT TTT AAT GCG ATG AAT AAG GCT TTA GAG AAT AAG	576
Ala Gly Asn Val Phe Phe Asn Ala Met Asn Lys Ala Leu Glu Asn Lys	
360 365 370	
AAT GGA ACT AGT AGT GCT AGT GGA ACT AGT GGT GCG ACT GGT TCA GAT	624
Asn Gly Thr Ser Ser Ala Ser Gly Thr Ser Gly Ala Thr Gly Ser Asp	
375 380 385	
GGT CAA ACT TAC TCC ACA CAA GCT ATC CAA TAC CTT CAA GGC CAA CAA	672
Gly Gln Thr Tyr Ser Thr Gln Ala Ile Gln Tyr Leu Gln Gly Gln Gln	
390 395 400	
AAT ATC TTA AAT AAC GCA GCG AAC TTG CTC AAG CAA GAT GAA TTG CTC	720
Asn Ile Leu Asn Asn Ala Ala Asn Leu Leu Lys Gln Asp Glu Leu Leu	
405 410 415 420	

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TTA GAA GCT TTC AAC TCT GCC GTA GCC GCC AAC ATT GGG AAT AAG GAA Leu Glu Ala Phe Asn Ser Ala Val Ala Ala Asn Ile Gly Asn Lys Glu 425 430 435	768
TTC AAT TCA GCC GCT TTT ACA GGT TTG GTG CAA GGC ATT ATT GAT CAA Phe Asn Ser Ala Ala Phe Thr Gly Leu Val Gln Gly Ile Ile Asp Gln 440 445 450	816
TCT CAA GCG GTT TAT AAC GAG CTC ACT AAA AAC ACC ATT AGC GGG AGT Ser Gln Ala Val Tyr Asn Glu Leu Thr Lys Asn Thr Ile Ser Gly Ser 455 460 465	864
GCG GTT ATT AGC GCT GGG ATA AAC TCC AAC CAA GCT AAC GCT GTG CAA Ala Val Ile Ser Ala Gly Ile Asn Ser Asn Gln Ala Asn Ala Val Gln 470 475 480	912
GGG CGC GCT AGT CAG CTC CCT AAC GCT CTT TAT AAC GCG CAA GTA ACT Gly Arg Ala Ser Gln Leu Pro Asn Ala Leu Tyr Asn Ala Gln Val Thr 485 490 495 500	960
TTG GAT AAA ATC AAT GCG CTC AAT AAT CAA GTG AGA AGC ATG CCT TAC Leu Asp Lys Ile Asn Ala Leu Asn Asn Gln Val Arg Ser Met Pro Tyr 505 510 515	1008
TTG CCC CAA TTC AGA GCC GGG AAC AGC CGT TCA ACG AAT ATT TTA AAC Leu Pro Gln Phe Arg Ala Gly Asn Ser Arg Ser Thr Asn Ile Leu Asn 520 525 530	1056
GGG TTT TAC ACC AAA ATA GGC TAT AAG CAA TTC TTC GGG AAG AAA AGG Gly Phe Tyr Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Lys Lys Arg 535 540 545	1104
AAT ATC GGT TTG CGC TAT TAT GGT TTC TTT TCT TAT AAC GGA GCG AGC Asn Ile Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala Ser 550 555 560	1152
GTG GGC TTT AGA TCC ACT CAA AAT AAT GTA GGG TTA TAC ACT TAT GGG Val Gly Phe Arg Ser Thr Gln Asn Asn Val Gly Leu Tyr Thr Tyr Gly 565 570 575 580	1200
GTG GGG ACT GAT GTG TTG TAT AAC ATC TTT AGC CGC TCC TAT CAA AAC Val Gly Thr Asp Val Leu Tyr Asn Ile Phe Ser Arg Ser Tyr Gln Asn 585 590 595	1248
CGC TCT GTG GAT ATG GGC TTT TTT AGC GGT ATC CAA TTA GCC GGT GAG Arg Ser Val Asp Met Gly Phe Phe Ser Gly Ile Gln Leu Ala Gly Glu 600 605 610	1296
ACC TTC CAA TCC ACG CTC AGA GAT GAC CCC AAT GTG AAA TTG CAT GGG Thr Phe Gln Ser Thr Leu Arg Asp Asp Pro Asn Val Lys Leu His Gly 615 620 625	1344
AAA ATC AAT AAC ACG CAC TTC CAG TTC CTC TTT GAC TTC GGT ATG AGG Lys Ile Asn Asn Thr His Phe Gln Phe Leu Phe Asp Phe Gly Met Arg 630 635 640	1392
ATG AAC TTC GGT AAG TTG GAC GGG AAA TCC AAC CGC CAC AAC CAG CAC Met Asn Phe Gly Lys Leu Asp Gly Lys Ser Asn Arg His Asn Gln His 645 650 655 660	1440

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ACG GTG GAA TTT GGC GTA GTG GTG CCT ACG ATT TAT AAC ACT TAT TAC	1488
Thr Val Glu Phe Gly Val Val Val Pro Thr Ile Tyr Asn Thr Tyr Tyr	
665 670 675	
AAA TCA GCA GGG ACT ACC GTG AAG TAT TTC CGT CCT TAT AGC GTT TAT	1536
Lys Ser Ala Gly Thr Thr Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr	
680 685 690	
TGG TCT TAT GGG TAT TCA TTC TAA	1560
Trp Ser Tyr Gly Tyr Ser Phe *	
695 700	

## (2) INFORMATION FOR SEQ ID NO: 48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Gln Met Ile Lys Lys Asn Arg Thr Leu Phe Leu Ser Leu Ala Leu Cys	
1 5 10 15	
Ala Ser Ile Ser Tyr Ala Glu Asp Asp Gly Gly Phe Phe Thr Val Gly	
20 25 30	
Tyr Gln Leu Gly Gln Val Met Gln Asp Val Gln Asn Pro Gly Gly Ala	
35 40 45	
Lys Ser Asp Glu Leu Ala Arg Glu Leu Asn Ala Asp Val Thr Asn Asn	
50 55 60	
Ile Leu Asn Asn Asn Thr Gly Gly Asn Ile Ala Gly Ala Leu Ser Asn	
65 70 75 80	
Ala Phe Ser Gln Tyr Leu Tyr Ser Leu Leu Gly Ala Tyr Pro Thr Lys	
85 90 95	
Leu Asn Gly Ser Asp Val Ser Ala Asn Ala Leu Leu Ser Gly Ala Val	
100 105 110	
Gly Ser Gly Thr Cys Ala Ala Ala Gly Thr Ala Gly Gly Thr Ser Leu	
115 120 125	
Asn Thr Gln Ser Thr Cys Thr Val Ala Gly Tyr Tyr Trp Leu Pro Ser	
130 135 140	
Leu Thr Asp Arg Ile Leu Ser Thr Ile Gly Ser Gln Thr Asn Tyr Gly	
145 150 155 160	
Thr Asn Thr Asn Phe Pro Asn Met Gln Gln Gln Leu Thr Tyr Leu Asn	
165 170 175	
Ala Gly Asn Val Phe Phe Asn Ala Met Asn Lys Ala Leu Glu Asn Lys	
180 185 190	

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Asn Gly Thr Ser Ser Ala Ser Gly Thr Ser Gly Ala Thr Gly Ser Asp  
195 200 205

Gly Gln Thr Tyr Ser Thr Gln Ala Ile Gln Tyr Leu Gln Gly Gln Gln  
210 215 220

Asn Ile Leu Asn Asn Ala Ala Asn Leu Leu Lys Gln Asp Glu Leu Leu  
225 230 235 240

Leu Glu Ala Phe Asn Ser Ala Val Ala Ala Asn Ile Gly Asn Lys Glu  
245 250 255

Phe Asn Ser Ala Ala Phe Thr Gly Leu Val Gln Gly Ile Ile Asp Gln  
260 265 270

Ser Gln Ala Val Tyr Asn Glu Leu Thr Lys Asn Thr Ile Ser Gly Ser  
275 280 285

Ala Val Ile Ser Ala Gly Ile Asn Ser Asn Gln Ala Asn Ala Val Gln  
290 295 300

Gly Arg Ala Ser Gln Leu Pro Asn Ala Leu Tyr Asn Ala Gln Val Thr  
305 310 315 320

Leu Asp Lys Ile Asn Ala Leu Asn Asn Gln Val Arg Ser Met Pro Tyr  
325 330 335

Leu Pro Gln Phe Arg Ala Gly Asn Ser Arg Ser Thr Asn Ile Leu Asn  
340 345 350

Gly Phe Tyr Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Lys Lys Arg  
355 360 365

Asn Ile Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala Ser  
370 375 380

Val Gly Phe Arg Ser Thr Gln Asn Asn Val Gly Leu Tyr Thr Tyr Gly  
385 390 395 400

Val Gly Thr Asp Val Leu Tyr Asn Ile Phe Ser Arg Ser Tyr Gln Asn  
405 410 415

Arg Ser Val Asp Met Gly Phe Phe Ser Gly Ile Gln Leu Ala Gly Glu  
420 425 430

Thr Phe Gln Ser Thr Leu Arg Asp Asp Pro Asn Val Lys Leu His Gly  
435 440 445

Lys Ile Asn Asn Thr His Phe Gln Phe Leu Phe Asp Phe Gly Met Arg  
450 455 460

Met Asn Phe Gly Lys Leu Asp Gly Lys Ser Asn Arg His Asn Gln His  
465 470 475 480

Thr Val Glu Phe Gly Val Val Val Pro Thr Ile Tyr Asn Thr Tyr Tyr  
485 490 495

Lys Ser Ala Gly Thr Thr Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr

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500

505

510

Trp Ser Tyr Gly Tyr Ser Phe \*  
 515 520

## (2) INFORMATION FOR SEQ ID NO: 49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS152

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1062

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TTG AAA CAT TTA ACC CCA CTC ACT CAC ACC ATC TTT AAA GCC TTA TGG	48
Leu Lys His Leu Thr Pro Leu Thr His Thr Ile Phe Lys Ala Leu Trp	
525 530 535	
CTA GGC ACA GCC TTA AGT GCA TCT TTA AGT TTA GCC GCA ACA GAA AGC	96
Leu Gly Thr Ala Leu Ser Ala Ser Leu Ser Leu Ala Ala Thr Glu Ser	
540 545 550	
CCC ACT AAA ACA GAG CCT AAG CCC GCT AAA GGG GTT AAA AAC AAG CCC	144
Pro Thr Lys Thr Glu Pro Lys Pro Ala Lys Gly Val Lys Asn Lys Pro	
555 560 565	
AAA TCG CCC GTT ACT AAA GTC ATG ATG ACC AAT TGC GAC AAT ATT AAA	192
Lys Ser Pro Val Thr Lys Val Met Met Thr Asn Cys Asp Asn Ile Lys	
570 575 580	
GAT TTT AAC GCT AAG CAA AAA GAA GTC TTA AAA GCC GCT TAT CAA TTC	240
Asp Phe Asn Ala Lys Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe	
585 590 595 600	
GGC TCT AAA GAA AAT TTA GGC TAT GAA ATG GCA GGC ATT GCA TGG AAA	288
Gly Ser Lys Glu Asn Leu Gly Tyr Glu Met Ala Gly Ile Ala Trp Lys	
605 610 615	
GAG TCA TGC GCA GGG GTT TAT AAA ATC AAT TTT TCG GAT CCG AGC GCG	336
Glu Ser Cys Ala Gly Val Tyr Lys Ile Asn Phe Ser Asp Pro Ser Ala	
620 625 630	
GGC GTG TAT CAT TCT TAT ATC CCA AGC GTT CTA AAA AGC TAT GGG CAT	384
Gly Val Tyr His Ser Tyr Ile Pro Ser Val Leu Lys Ser Tyr Gly His	
635 640 645	
AAT GAT AGC CCC TTT TTG CGT AAT GTG ATG GGG GAA TTG CTC ATT AAA	432
Asn Asp Ser Pro Phe Leu Arg Asn Val Met Gly Glu Leu Leu Ile Lys	

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650	655	660	
GAC GAT GCG TTT GCT TCT GAA GTG GCT TTA AAA GAG TTG CTC TAT TGG			480
Asp Asp Ala Phe Ala Ser Glu Val Ala Leu Lys Glu Leu Leu Tyr Trp			
665	670	675	680
AAA ACA CGC TAC CAT GAC AAT TTA AAA GAC ATG ATT AAA TCT TAC AAC			528
Lys Thr Arg Tyr His Asp Asn Leu Lys Asp Met Ile Lys Ser Tyr Asn			
	685	690	695
AAG GGC AGT CGT TGG GAA AGG AGC GAA AAA TCT AAC GCT GAT GCT GAA			576
Lys Gly Ser Arg Trp Glu Arg Ser Glu Lys Ser Asn Ala Asp Ala Glu			
	700	705	710
AAA TAT TAC GAA GAG ATA CAA GAC AGA ATC AGG CGT TTG AAA GAA TCT			624
Lys Tyr Tyr Glu Glu Ile Gln Asp Arg Ile Arg Arg Leu Lys Glu Ser			
	715	720	725
AAA ATC TTT GAT TCG CAG TCT AGT AAT GAC CAA GAA TTG CAA AAA AGC			672
Lys Ile Phe Asp Ser Gln Ser Ser Asn Asp Gln Glu Leu Gln Lys Ser			
	730	735	740
GCT AAT AGC AAC CTG GAT TTA GAC CCT ATC GGC AAC GCC ATG CCC CAA			720
Ala Asn Ser Asn Leu Asp Leu Asp Pro Ile Gly Asn Ala Met Pro Gln			
	745	750	755
GCC TTA ATT GCC AAA GAA ACT AAA ATA GAA GAA ACC CAA GCA GAA AAA			768
Ala Leu Ile Ala Lys Glu Thr Lys Ile Glu Glu Thr Gln Ala Glu Lys			
	765	770	775
TCC CAA GAA ATG AAA GAG ACA ACT AGC GAG CAA ACA AAA AGT AAG CCA			816
Ser Gln Glu Met Lys Glu Thr Thr Ser Glu Gln Thr Lys Ser Lys Pro			
	780	785	790
GAA AAA GCA AAA GAT AAA CCC ATG TAT TTG GCG CAA ATC AAC AGC ACT			864
Glu Lys Ala Lys Asp Lys Pro Met Tyr Leu Ala Gln Ile Asn Ser Thr			
	795	800	805
GAT TTC ACA CCC GTT AAA AAA AGC CCC AAA AAA CCG GCT AAA GTG AGC			912
Asp Phe Thr Pro Val Lys Lys Ser Pro Lys Lys Pro Ala Lys Val Ser			
	810	815	820
CAA AAA CAC TCC TTT AAG AAT AAC ATT AAA AAT AAT GTA AAA AAC AAC			960
Gln Lys His Ser Phe Lys Asn Asn Ile Lys Asn Asn Val Lys Asn Asn			
	825	830	835
GCC AAA ACC GCT TCC AAA AAA CAA GAA ATG TGC AAA AAT TGC TCT CCA			1008
Ala Lys Thr Ala Ser Lys Lys Gln Glu Met Cys Lys Asn Cys Ser Pro			
	845	850	855
GGG CAA AGG AAT GCG ATT TTA GCT AAC CAC ATC ACT CTC ATG CAA GAG			1056
Gly Gln Arg Asn Ala Ile Leu Ala Asn His Ile Thr Leu Met Gln Glu			
	860	865	870
CTT TAA			1062
Leu *			

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## (2) INFORMATION FOR SEQ ID NO: 50:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 Amino acids

(B) TYPE: Amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Leu Lys His Leu Thr Pro Leu Thr His Thr Ile Phe Lys Ala Leu Trp  
 1 5 10 15  
 Leu Gly Thr Ala Leu Ser Ala Ser Leu Ser Leu Ala Ala Thr Glu Ser  
 20 25 30  
 Pro Thr Lys Thr Glu Pro Lys Pro Ala Lys Gly Val Lys Asn Lys Pro  
 35 40 45  
 Lys Ser Pro Val Thr Lys Val Met Met Thr Asn Cys Asp Asn Ile Lys  
 50 55 60  
 Asp Phe Asn Ala Lys Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe  
 65 70 75 80  
 Gly Ser Lys Glu Asn Leu Gly Tyr Glu Met Ala Gly Ile Ala Trp Lys  
 85 90 95  
 Glu Ser Cys Ala Gly Val Tyr Lys Ile Asn Phe Ser Asp Pro Ser Ala  
 100 105 110  
 Gly Val Tyr His Ser Tyr Ile Pro Ser Val Leu Lys Ser Tyr Gly His  
 115 120 125  
 Asn Asp Ser Pro Phe Leu Arg Asn Val Met Gly Glu Leu Leu Ile Lys  
 130 135 140  
 Asp Asp Ala Phe Ala Ser Glu Val Ala Leu Lys Glu Leu Leu Tyr Trp  
 145 150 155 160  
 Lys Thr Arg Tyr His Asp Asn Leu Lys Asp Met Ile Lys Ser Tyr Asn  
 165 170 175  
 Lys Gly Ser Arg Trp Glu Arg Ser Glu Lys Ser Asn Ala Asp Ala Glu  
 180 185 190  
 Lys Tyr Tyr Glu Glu Ile Gln Asp Arg Ile Arg Arg Leu Lys Glu Ser  
 195 200 205  
 Lys Ile Phe Asp Ser Gln Ser Ser Asn Asp Gln Glu Leu Gln Lys Ser  
 210 215 220  
 Ala Asn Ser Asn Leu Asp Leu Asp Pro Ile Gly Asn Ala Met Pro Gln  
 225 230 235 240  
 Ala Leu Ile Ala Lys Glu Thr Lys Ile Glu Glu Thr Gln Ala Glu Lys  
 245 250 255  
 Ser Gln Glu Met Lys Glu Thr Thr Ser Glu Gln Thr Lys Ser Lys Pro

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260 265 270

Glu Lys Ala Lys Asp Lys Pro Met Tyr Leu Ala Gln Ile Asn Ser Thr  
275 280 285

Asp Phe Thr Pro Val Lys Lys Ser Pro Lys Lys Pro Ala Lys Val Ser  
290 295 300

Gln Lys His Ser Phe Lys Asn Asn Ile Lys Asn Asn Val Lys Asn Asn  
305 310 315 320

Ala Lys Thr Ala Ser Lys Lys Gln Glu Met Cys Lys Asn Cys Ser Pro  
325 330 335

Gly Gln Arg Asn Ala Ile Leu Ala Asn His Ile Thr Leu Met Gln Glu  
340 345 350

Leu \*

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2202 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS155

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..2202

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ATG GCA AAC GAA CGC TCC AAA TTA GCT TTT AAA AAG ACT TTC CCT GTC	48
Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val	
355 360 365 370	
TTT AAA CGC TTT TTG CAA TCC AAA GAC TTA GCC CTT GTG GTC TTT GTG	96
Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val	
375 380 385	
ATC GCT ATT TTG GCG ATC ATT ATC GTG CCG TTA CCG CCT TTT GTG TTG	144
Ile Ala Ile Leu Ala Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu	
390 395 400	
GAT TTT TTA CTC ACG ATT TCT ATC GCG CTG TCG GTG TTG ATT ATT TTA	192
Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu	
405 410 415	
ATT GGG CTT TAT ATT GAC AAG CCG ACT GAT TTT AGC GCT TTC CCC ACT	240
Ile Gly Leu Tyr Ile Asp Lys Pro Thr Asp Phe Ser Ala Phe Pro Thr	
420 425 430	

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TTA TTG CTC ATT GTA ACC TTG TAT CGC TTG GCT TTA AAT GTC GCC ACC	288
Leu Leu Leu Ile Val Thr Leu Tyr Arg Leu Ala Leu Asn Val Ala Thr	
435 440 445 450	
ACT AGA ATG ATT TTA ACG CAA GGC TAT AAA GGG CCT AGT GCG GTG AGC	336
Thr Arg Met Ile Leu Thr Gln Gly Tyr Lys Gly Pro Ser Ala Val Ser	
455 460 465	
GAT ATT ATC ACG GCG TTT GGG GAA TTT AGC GTG AGC GGG AAT TAT GTG	384
Asp Ile Ile Thr Ala Phe Gly Glu Phe Ser Val Ser Gly Asn Tyr Val	
470 475 480	
ATT GGG GCG ATT ATC TTT AGT ATT TTA GTG CTA GTG AAT CTA TTA GTG	432
Ile Gly Ala Ile Ile Phe Ser Ile Leu Val Leu Val Asn Leu Leu Val	
485 490 495	
GTT ACT AAT GGC TCT ACT AGG GTT ACT GAA GTG AGG GCG CGA TTT GCC	480
Val Thr Asn Gly Ser Thr Arg Val Thr Glu Val Arg Ala Arg Phe Ala	
500 505 510	
CTA GAT GCT ATG CCA GGA AAG CAA ATG GCG ATT GAT GCG GAT TTA AAC	528
Leu Asp Ala Met Pro Gly Lys Gln Met Ala Ile Asp Ala Asp Leu Asn	
515 520 525 530	
TCA GGA CTT ATT GAC GAT AAG GAA GCC AAA AAA CGG CGC GCC GCT CTA	576
Ser Gly Leu Ile Asp Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu	
535 540 545	
AGC CAA GAA GCG GAT TTT TAT GGC GCG ATG GAT GGC GCA TCT AAA TTC	624
Ser Gln Glu Ala Asp Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe	
550 555 560	
GTC AAA GGC GAT GCG ATC GCT TCT ATC ATC ATC ACG CTT ATC AAT ATC	672
Val Lys Gly Asp Ala Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile	
565 570 575	
ATT GGA GGG TTT TTA GTG GGC GTG TTT CAA AGG GAT ATG AGC TTG AGC	720
Ile Gly Gly Phe Leu Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser	
580 585 590	
TTT AGC GCT AGC ACT TTC ACT ATC TTA ACC ATT GGC GAT GGG CTT GTG	768
Phe Ser Ala Ser Thr Phe Thr Ile Leu Thr Ile Gly Asp Gly Leu Val	
595 600 605 610	
GGG CAA ATC CCT GCC TTA ATC ATT GCG ACA GCG ACC GGT ATT GTC GCC	816
Gly Gln Ile Pro Ala Leu Ile Ile Ala Thr Ala Thr Gly Ile Val Ala	
615 620 625	
ACT CGC ACC ACG CAA AAT GAA GAA GAG GAC TTT GCT TCC AAA CTC ATC	864
Thr Arg Thr Thr Gln Asn Glu Glu Glu Asp Phe Ala Ser Lys Leu Ile	
630 635 640	
ACA CAG CTC ACC AAT AAA AGC AAA ACT TTA GTG ATT GTG GGA GCG ATT	912
Thr Gln Leu Thr Asn Lys Ser Lys Thr Leu Val Ile Val Gly Ala Ile	
645 650 655	
TTA TTG CTT TTT GCC ACC ATT CCT GGA CTC CCT ACC TTT TCT TTA GCG	960
Leu Leu Leu Phe Ala Thr Ile Pro Gly Leu Pro Thr Phe Ser Leu Ala	

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660	665	670	
TTT GTA GGG ACT CTC TTT TTA TTC ATC GCA TGG CTG ATT AGC AGG GAG	1008		
Phe Val Gly Thr Leu Phe Leu Phe Ile Ala Trp Leu Ile Ser Arg Glu			
675 680 685 690			
GGG AAA GAC GGG CTG CTC ACT AAA TTA GAA AAT TAT TTG AGT CAA AAA	1056		
Gly Lys Asp Gly Leu Leu Thr Lys Leu Glu Asn Tyr Leu Ser Gln Lys			
695 700 705			
TTC GGC TTG GAT TTG AGC GAA AAA CCC CAC AGC TCC AAA ATC AAA CCC	1104		
Phe Gly Leu Asp Leu Ser Glu Lys Pro His Ser Ser Lys Ile Lys Pro			
710 715 720			
CAC ACC CCA ACC ACA AGG GCT AAA ACC CAA GAA GAG CTT AAA AGA GAA	1152		
His Thr Pro Thr Thr Arg Ala Lys Thr Gln Glu Glu Leu Lys Arg Glu			
725 730 735			
GAA GAG CAA GCG ATT GAT GAA GTG TTA AAA ATT GAA TTT TTA GAA CTG	1200		
Glu Glu Gln Ala Ile Asp Glu Val Leu Lys Ile Glu Phe Leu Glu Leu			
740 745 750			
GCT TTA GGC TAT CAA CTC ATC AGT CTT GCG GAC ATG AAA CAA GGG GGC	1248		
Ala Leu Gly Tyr Gln Leu Ile Ser Leu Ala Asp Met Lys Gln Gly Gly			
755 760 765 770			
GAT TTG TTA GAA AGG ATT AGG GGT ATT AGA AAA AAG ATA GCG AGC GAT	1296		
Asp Leu Leu Glu Arg Ile Arg Gly Ile Arg Lys Lys Ile Ala Ser Asp			
775 780 785			
TAT GGT TTT TTG ATG CCT CAA ATC CGG ATC AGG GAT AAT TTG CAG CTC	1344		
Tyr Gly Phe Leu Met Pro Gln Ile Arg Ile Arg Asp Asn Leu Gln Leu			
790 795 800			
CCC CCA ACG CAT TAT GAA ATC AAA CTT AAA GGC ATT GTG ATT GGT GAG	1392		
Pro Pro Thr His Tyr Glu Ile Lys Leu Lys Gly Ile Val Ile Gly Glu			
805 810 815			
GGC ATG GTG ATG CCA GAC AAG TTT TTA GCC ATG AAT ACC GGT TTT GTG	1440		
Gly Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val			
820 825 830			
AAT AAA GAA ATT GAA GGC ATT CCT ACT AAA GAG CCG GCT TTT GGA ATG	1488		
Asn Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met			
835 840 845 850			
GAC GCT TTA TGG ATT GAA ACT AAA AAT AAA GAA GAA GCC ATT ATT CAA	1536		
Asp Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln			
855 860 865			
GGC TAT ACC ATT ATT GAT CCA AGC ACC GTT ATT GCG ACG CAC ACC AGC	1584		
Gly Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser			
870 875 880			
GAA TTA GTG AAA AAA TAC GCT GAA GAT TTT ATC ACT AAA GAT GAA GTG	1632		
Glu Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val			
885 890 895			
AAA TCC CTT TTA GAG CGC TTG GCC AAA GAT TAT CCT ACG ATT GTA GAA	1680		

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Lys Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu  
 900 905 910

GAG AGT AAA AAA ATC CCC ACC GGT GCG ATC CGA TCA GTC TTG CAA GCC 1728  
 Glu Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala  
 915 920 925 930

TTG TTA CAT GAA AAA ATC CCC ATT AAA GAC ATG CTC ACT ATT TTA GAA 1776  
 Leu Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu  
 935 940 945

ACG ATT ACC GAT ATT GCC CCA TTG GTT CAA AAC GAT GTG AAT ATC TTA 1824  
 Thr Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu  
 950 955 960

ACC GAA CAA GTG AGG GCG AGG CTT TCT AGG GTG ATC ACT AAC GCT TTT 1872  
 Thr Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe  
 965 970 975

AAA TCT GAA GAC GGG CGT TTG AAA TTT TTA ACC TTT TCT ACC GAT AGC 1920  
 Lys Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser  
 980 985 990

GAA CAA TTT TTG CTT AAT AAA TTG CGA GAA AAT GGC ACT TCT AAA AGT 1968  
 Glu Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser  
 995 1000 1005 1010

TTG CTG CTC AAT GTG GGC GAA TTG CAA AAA CTC ATT GAA GTG GTC TCT 2016  
 Leu Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Val Val Ser  
 1015 1020 1025

GAA GAG GCC ATG AAA GTC TTG CAA AAA GGG ATC GCT CCG GTG ATT TTG 2064  
 Glu Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu  
 1030 1035 1040

ATC GTA GAG CCT AAT TTA AGA AAA GCT CTT TCC AAT CAA ATG GAG CAA 2112  
 Ile Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln  
 1045 1050 1055

GCC AGG ATT GAT GTG ATC GTG CTA AGC CAT GCG GAA TTA GAT CCT AAC 2160  
 Ala Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn  
 1060 1065 1070

TCT AAT TTT GAA GCT TTA GGC ACG ATC CAT ATT AAC TTT TAA 2202  
 Ser Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe \*  
 1075 1080 1085

## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val

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1	5	10	15
Phe Lys Arg	Phe Leu Gln Ser Lys	Asp Leu Ala Leu Val	Val Phe Val
	20	25	30
Ile Ala Ile	Leu Ala Ile Ile Ile	Val Pro Leu Pro Pro	Phe Val Leu
	35	40	45
Asp Phe Leu	Leu Thr Ile Ser Ile Ala Leu	Ser Val Leu Ile Ile	Leu
	50	55	60
Ile Gly Leu	Tyr Ile Asp Lys Pro Thr	Asp Phe Ser Ala Phe	Pro Thr
	65	70	75 80
Leu Leu Leu	Ile Val Thr Leu Tyr Arg	Leu Ala Leu Asn Val	Ala Thr
	85	90	95
Thr Arg Met	Ile Leu Thr Gln Gly Tyr Lys	Gly Pro Ser Ala Val	Ser
	100	105	110
Asp Ile Ile	Thr Ala Phe Gly Glu Phe Ser	Val Ser Gly Asn Tyr	Val
	115	120	125
Ile Gly Ala	Ile Ile Phe Ser Ile Leu Val	Leu Val Asn Leu Leu	Val
	130	135	140
Val Thr Asn	Gly Ser Thr Arg Val Thr Glu	Val Arg Ala Arg Phe	Ala
	145	150	155 160
Leu Asp Ala	Met Pro Gly Lys Gln Met Ala	Ile Asp Ala Asp Leu	Asn
	165	170	175
Ser Gly Leu	Ile Asp Asp Lys Glu Ala Lys	Lys Arg Arg Ala Ala	Leu
	180	185	190
Ser Gln Glu	Ala Asp Phe Tyr Gly Ala Met	Asp Gly Ala Ser Lys	Phe
	195	200	205
Val Lys Gly	Asp Ala Ile Ala Ser Ile Ile	Ile Thr Leu Ile Asn	Ile
	210	215	220
Ile Gly Gly	Phe Leu Val Gly Val Phe Gln	Arg Asp Met Ser Leu	Ser
	225	230	235 240
Phe Ser Ala	Ser Thr Phe Thr Ile Leu Thr	Ile Gly Asp Gly Leu	Val
	245	250	255
Gly Gln Ile	Pro Ala Leu Ile Ile Ala Thr	Ala Thr Gly Ile Val	Ala
	260	265	270
Thr Arg Thr	Thr Gln Asn Glu Glu Glu Asp	Phe Ala Ser Lys Leu	Ile
	275	280	285
Thr Gln Leu	Thr Asn Lys Ser Lys Thr Leu	Val Ile Val Gly Ala	Ile
	290	295	300
Leu Leu Leu	Phe Ala Thr Ile Pro Gly Leu	Pro Thr Phe Ser Leu	Ala
	305	310	315 320

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Phe Val Gly Thr Leu Phe Leu Phe Ile Ala Trp Leu Ile Ser Arg Glu  
325 330 335

Gly Lys Asp Gly Leu Leu Thr Lys Leu Glu Asn Tyr Leu Ser Gln Lys  
340 345 350

Phe Gly Leu Asp Leu Ser Glu Lys Pro His Ser Ser Lys Ile Lys Pro  
355 360 365

His Thr Pro Thr Thr Arg Ala Lys Thr Gln Glu Glu Leu Lys Arg Glu  
370 375 380

Glu Glu Gln Ala Ile Asp Glu Val Leu Lys Ile Glu Phe Leu Glu Leu  
385 390 395 400

Ala Leu Gly Tyr Gln Leu Ile Ser Leu Ala Asp Met Lys Gln Gly Gly  
405 410 415

Asp Leu Leu Glu Arg Ile Arg Gly Ile Arg Lys Lys Ile Ala Ser Asp  
420 425 430

Tyr Gly Phe Leu Met Pro Gln Ile Arg Ile Arg Asp Asn Leu Gln Leu  
435 440 445

Pro Pro Thr His Tyr Glu Ile Lys Leu Lys Gly Ile Val Ile Gly Glu  
450 455 460

Gly Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val  
465 470 475 480

Asn Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met  
485 490 495

Asp Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln  
500 505 510

Gly Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser  
515 520 525

Glu Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val  
530 535 540

Lys Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu  
545 550 555 560

Glu Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala  
565 570 575

Leu Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu  
580 585 590

Thr Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu  
595 600 605

Thr Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe  
610 615 620

Lys Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser  
625 630 635 640

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Glu Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser  
                                 645                                650                                655  
 Leu Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Val Val Ser  
                                 660                                665                                670  
 Glu Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu  
                                 675                                680                                685  
 Ile Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln  
                                 690                                695                                700  
 Ala Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn  
                                 705                                710                                715                                720  
 Ser Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe \*  
                                 725                                730

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPC157 (HPC181)

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..189

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ATG CAA AAA GAA CAA GAA GCC CGA GAA ATC GCT AAA AAA GCC GTT CAA	48
Met Gln Lys Glu Gln Glu Ala Arg Glu Ile Ala Lys Lys Ala Val Gln	
735                                740                                745                                750	
ATC GTG TTT TTT TTA GGG ATT GTG GTG GTG CTT TTG ATG ATG ATA AAC	96
Ile Val Phe Phe Leu Gly Ile Val Val Val Leu Leu Met Met Ile Asn	
755                                760                                765	
CTT TAC ATG CTC ATC AAT CAA ATC AAC GCG AGC GCT AAA ATG AGC CAA	144
Leu Tyr Met Leu Ile Asn Gln Ile Asn Ala Ser Ala Lys Met Ser Gln	
770                                775                                780	
CAA ATC AAA AAA ATA GAA GAA AGG CTT AAC CAA GGG CAA AAA TAG	189
Gln Ile Lys Lys Ile Glu Glu Arg Leu Asn Gln Gly Gln Lys *	
785                                790                                795	

## (2) INFORMATION FOR SEQ ID NO: 54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

Met Gln Lys Glu Gln Glu Ala Arg Glu Ile Ala Lys Lys Ala Val Gln
 1             5             10             15

Ile Val Phe Phe Leu Gly Ile Val Val Val Leu Leu Met Met Ile Asn
          20             25             30

Leu Tyr Met Leu Ile Asn Gln Ile Asn Ala Ser Ala Lys Met Ser Gln
          35             40             45

Gln Ile Lys Lys Ile Glu Glu Arg Leu Asn Gln Gly Gln Lys *
 50             55             60
  
```

- (2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1008 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

- (vii) DIRECT SOURCE:  
 (B) CLONE(S): HPS183

- (ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) POSITION:1..1008

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

ATG TTA GTT ACT CGC TTT AAA AAA GCT TTC ATT TCT TAT TCT TTA GGC      48
Met Leu Val Thr Arg Phe Lys Lys Ala Phe Ile Ser Tyr Ser Leu Gly
 65             70             75

GTG CTT GTC GCT TCA TTA TGG TTG AAC GTG TGC AAC GCT TCA GCG CAA      96
Val Leu Val Ala Ser Leu Trp Leu Asn Val Cys Asn Ala Ser Ala Gln
 80             85             90             95

GAA GTC AAA GTC AAG GAT TAT TTC GGG GAG CAA ACC ATC AAG CTT CCT      144
Glu Val Lys Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro
          100             105             110

GTT TCT AAA ATA GCC TAT ATA GGG AGC TAT GTA GAA GTG CCT GCC ATG      192
Val Ser Lys Ile Ala Tyr Ile Gly Ser Tyr Val Glu Val Pro Ala Met
          115             120             125

CTT AAT GTT TGG AAT AGG GTT GTA GGC GTT TCG GAT TAC GCT TTT AAA      240
Leu Asn Val Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys
          130             135             140
  
```

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GAC GAT ATT GTC AAA GCC ACT CTC AAA GGC GAA GAT CTT AAA CGC GTC Asp Asp Ile Val Lys Ala Thr Leu Lys Gly Glu Asp Leu Lys Arg Val 145 150 155	288
AAA CAC ATG AGC ACT GAT CAT ACA GCC GCG CTA AAT GTA GAG CTT TTA Lys His Met Ser Thr Asp His Thr Ala Ala Leu Asn Val Glu Leu Leu 160 165 170 175	336
AAA AAG CTT AGC CCT GAT CTT GTG GTA ACC TTT GTG GGC AAC CCT AAA Lys Lys Leu Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys 180 185 190	384
GCG GTA GAG CAT GCG AAA AAA TTT GGT ATA TCA TTT CTT TCT TTT CAA Ala Val Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln 195 200 205	432
GAG ACA ACG ATT GCA GAG GCC ATG CAG GCC ATG CAA GCT CAA GCC ACG Glu Thr Thr Ile Ala Glu Ala Met Gln Ala Met Gln Ala Gln Ala Thr 210 215 220	480
GTT TTA GAG ATT GAC GCT TCC AAA AAA TTC GCC AAA ATG CAA GAA ACT Val Leu Glu Ile Asp Ala Ser Lys Lys Phe Ala Lys Met Gln Glu Thr 225 230 235	528
TTG GAT TTT ATT GCT GAG CGT TTG AAA AAT GTC AAA AAG AAA AAG GGG Leu Asp Phe Ile Ala Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly 240 245 250 255	576
GTG GAG CTT TTC CAT AAA GCC AAT AAA ATC AGC GGC CAT CAA GCC ATT Val Glu Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile 260 265 270	624
AGC TCA GAC ATT TTA GAA AAA GGG GGC ATA GAC AAT TTT GGC TTG AAA Ser Ser Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys 275 280 285	672
TAT GTC AAA TTT GGG CGT GCT GAC ATT AGC GTG GAA AAA ATC GTT AAA Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys 290 295 300	720
GAA AAC CCT GAG ATT ATC TTT ATT TGG TGG ATA AGC CCA CTC ACG CCT Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro 305 310 315	768
GAA GAT GTG TTA AAC AAC CCC AAA TTT GCT ACC ATC AAA GCC ATT AAA Glu Asp Val Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys 320 325 330 335	816
AAC AAG CAG GTT TAT AAA CTC CCC ACA ATG GAT ATT GGC GGG CCT AGA Asn Lys Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg 340 345 350	864
GCC CCA CTC ATA AGT CTT TTT ATC GCT CTA AAA GCC CAC CCT GAA GCC Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala 355 360 365	912
TTT AAG GGC GTG GAT ATT AAT GCG ATG GTT AAA GAC TAC TAT AAA GTG Phe Lys Gly Val Asp Ile Asn Ala Met Val Lys Asp Tyr Tyr Lys Val 370 375 380	960

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GTT TTT GAT TTG AAT GAT GCA GAG GTT GAG CCC TTT TTA TGG CAT TAA  
 Val Phe Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His \*  
 385 390 395

1008

## (2) INFORMATION FOR SEQ ID NO: 56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Met Leu Val Thr Arg Phe Lys Lys Ala Phe Ile Ser Tyr Ser Leu Gly  
 1 5 10 15  
 Val Leu Val Ala Ser Leu Trp Leu Asn Val Cys Asn Ala Ser Ala Gln  
 20 25 30  
 Glu Val Lys Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro  
 35 40 45  
 Val Ser Lys Ile Ala Tyr Ile Gly Ser Tyr Val Glu Val Pro Ala Met  
 50 55 60  
 Leu Asn Val Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys  
 65 70 75 80  
 Asp Asp Ile Val Lys Ala Thr Leu Lys Gly Glu Asp Leu Lys Arg Val  
 85 90 95  
 Lys His Met Ser Thr Asp His Thr Ala Ala Leu Asn Val Glu Leu Leu  
 100 105 110  
 Lys Lys Leu Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys  
 115 120 125  
 Ala Val Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln  
 130 135 140  
 Glu Thr Thr Ile Ala Glu Ala Met Gln Ala Met Gln Ala Gln Ala Thr  
 145 150 155 160  
 Val Leu Glu Ile Asp Ala Ser Lys Lys Phe Ala Lys Met Gln Glu Thr  
 165 170 175  
 Leu Asp Phe Ile Ala Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly  
 180 185 190  
 Val Glu Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile  
 195 200 205  
 Ser Ser Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys  
 210 215 220  
 Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys

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(2) INFORMATION FOR SEQ ID NO: 57:

(A) LENGTH: 240 Base pairs  
(B) TYPE: Nucleotide  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(B) CLONE(S): HPS186

(A) NAME/KEY: CDS  
(B) POSITION: 1..240

ATG	GGC	GGA	TTC	ACA	AGC	ATA	TGG	CAT	TGG	GTC	ATT	GTT	TTA	TTA	GTG	48
Met	Gly	Gly	Phe	Thr	Ser	Ile	Trp	His	Trp	Val	Ile	Val	Leu	Leu	Val	
			340					345					350			
ATT	GTG	TTG	TTA	TTT	GGG	GCT	AAA	AAG	ATC	CCA	GAA	TTG	GCT	AAA	GGT	96
Ile	Val	Leu	Leu	Phe	Gly	Ala	Lys	Lys	Ile	Pro	Glu	Leu	Ala	Lys	Gly	
			355				360					365				
TTA	GGC	AGT	GGG	ATT	AAG	AAT	TTC	AAA	AAA	GCC	GTG	AAA	GAC	GAT	GAA	144
Leu	Gly	Ser	Gly	Ile	Lys	Asn	Phe	Lys	Lys	Ala	Val	Lys	Asp	Asp	Glu	
			370			375					380					
GAA	GAG	GCT	AAA	AAC	GAG	CCA	AAA	ACC	CTA	GAC	GCT	CAA	GCA	ACG	CAA	192
Glu	Glu	Ala	Lys	Asn	Glu	Pro	Lys	Thr	Leu	Asp	Ala	Gln	Ala	Thr	Gln	
					390					395					400	
ACC	AAA	GTG	CAT	GAG	AGT	AGC	GAG	ATT	AAA	AGC	AAA	CAA	GAA	AGT	TAA	240
Thr	Lys	Val	His	Glu	Ser	Ser	Glu	Ile	Lys	Ser	Lys	Gln	Glu	Ser	*	



405

410

415

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val
 1           5           10           15

Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly
          20           25           30

Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu
          35           40           45

Glu Glu Ala Lys Asn Glu Pro Lys Thr Leu Asp Ala Gln Ala Thr Gln
          50           55           60

Thr Lys Val His Glu Ser Ser Glu Ile Lys Ser Lys Gln Glu Ser *
65           70           75           80

```

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1764 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS188

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..1764

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ATG AAA AAC TTT TCC CCA CTT TGT TGT TTT AAA AAG CTC AAA AAA CGC      48
Met Lys Asn Phe Ser Pro Leu Cys Cys Phe Lys Lys Leu Lys Lys Arg
          85           90           95

CAT TTA ATC GCT TTG AGC CTG CCC TTG CTT TCT TAT GCT AAT GGC TTT      96
His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala Asn Gly Phe
          100          105          110

AAA ATC CAA GAG CAA AGC CTG AAT GGC ACG GCT TTA GGC TCG GCG TAT .... 144
Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly Ser Ala Tyr

```

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115	120	125	
GTC GCT GGG GCT AGG GGG GCT GAT GCT TCC TTT TAT AAC CCG GCG AAT Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn Pro Ala Asn 130 135 140			192
ATG GGC TTT ACT AAC GAT TGG GAT GAA AAC AGA AGC GAA TTT GAA ATG Met Gly Phe Thr Asn Asp Trp Asp Glu Asn Arg Ser Glu Phe Glu Met 145 150 155 160			240
ACC ACC ACC GTG ATT AAT ATC CCG GCC TTT AAG TTT CAA GTC CCT ACG Thr Thr Thr Val Ile Asn Ile Pro Ala Phe Lys Phe Gln Val Pro Thr 165 170 175			288
ACT AAT CAA GGC TTG TAT TCG GTT ACG AGC TTA CAA ATT GAT AAA AGC Thr Asn Gln Gly Leu Tyr Ser Val Thr Ser Leu Gln Ile Asp Lys Ser 180 185 190			336
CAA CAA AAT ATT TTA GGC ATC ATC AAC ACT ATA GGG CTT AGC AAT ATC Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu Ser Asn Ile 195 200 205			384
CTT AAA GCG CTT GGC AAT ACG GCC GCT ACC AAT GGC TTA TCA CAA GCA Leu Lys Ala Leu Gly Asn Thr Ala Ala Thr Asn Gly Leu Ser Gln Ala 210 215 220			432
ATC AAT CGG GTT CAA GGG CTT ATG AAT CTA ACC AAT CAA AAA GTC GTA Ile Asn Arg Val Gln Gly Leu Met Asn Leu Thr Asn Gln Lys Val Val 225 230 235 240			480
ACC CTC GCT TCA AAA CCT GAC ACC CAA ATC GTG AAT GGC TGG ACG GGA Thr Leu Ala Ser Lys Pro Asp Thr Gln Ile Val Asn Gly Trp Thr Gly 245 250 255			528
ACG ACT AAT TTT GTT TTA CCC AAA TTC TTT TAT AAA ACG CGC ACG CAT Thr Thr Asn Phe Val Leu Pro Lys Phe Phe Tyr Lys Thr Arg Thr His 260 265 270			576
AAC GGC TTC ACT TTT GGG GGG AGT TTT ACC GCT CCT AGC GGG TTG GGC Asn Gly Phe Thr Phe Gly Gly Ser Phe Thr Ala Pro Ser Gly Leu Gly 275 280 285			624
ATG AAA TGG AAT GGT AAA GGG GGG GAA TTT TTG CAT GAC GTG TTT ATC Met Lys Trp Asn Gly Lys Gly Gly Glu Phe Leu His Asp Val Phe Ile 290 295 300			672
ATG ATG GTA GAG CTT GCC CCT AGC ATG AGC TAT ACT GTT AAT AAG CAC Met Met Val Glu Leu Ala Pro Ser Met Ser Tyr Thr Val Asn Lys His 305 310 315 320			720
TTT TCC GTG GGC GTG GGC TTA AGG GGG CTT TAT GCG ACC GGG AGC TTT Phe Ser Val Gly Val Gly Leu Arg Gly Leu Tyr Ala Thr Gly Ser Phe 325 330 335			768
AAT AAC ACC GTT TAT GTG CCT TTA GAG GGC GCT TCG GTT TTG AGC GCG Asn Asn Thr Val Tyr Val Pro Leu Glu Gly Ala Ser Val Leu Ser Ala 340 345 350			816
GAG CAA ATT TTA AAT TTA CCC AAC AAT GTT TTT GCC GAT CAA GTG CCA			864

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Glu	Gln	Ile	Leu	Asn	Leu	Pro	Asn	Asn	Val	Phe	Ala	Asp	Gln	Val	Pro	
			355				360					365				
AGT	AAC	ATG	ATG	ACT	TTA	TTA	GGC	AAT	ATT	GGC	TAC	CAA	CCA	GCG	CTT	912
Ser	Asn	Met	Met	Thr	Leu	Leu	Gly	Asn	Ile	Gly	Tyr	Gln	Pro	Ala	Leu	
		370					375				380					
AAT	TGC	CAA	AAA	GCC	GGT	GGG	GAT	ATG	AGC	GAT	CAG	AGC	TGT	CAA	GAG	960
Asn	Cys	Gln	Lys	Ala	Gly	Gly	Asp	Met	Ser	Asp	Gln	Ser	Cys	Gln	Glu	
		385				390				395					400	
TTT	TAT	AAC	GGC	TTG	AAA	AAA	ATC	ATG	GGC	TAT	AGC	GGC	TTA	ATC	AAA	1008
Phe	Tyr	Asn	Gly	Leu	Lys	Lys	Ile	Met	Gly	Tyr	Ser	Gly	Leu	Ile	Lys	
				405					410					415		
GCG	AGC	GCG	AAT	CTT	TAT	GGC	ACG	ACT	CAA	GTC	GTG	CAA	AAA	TCT	AAC	1056
Ala	Ser	Ala	Asn	Leu	Tyr	Gly	Thr	Thr	Gln	Val	Val	Gln	Lys	Ser	Asn	
			420					425					430			
GGG	CAA	GGC	GTA	TCG	GGG	GGC	TAT	AGA	GTG	GGT	TCG	AGT	TTG	CGT	GTG	1104
Gly	Gln	Gly	Val	Ser	Gly	Gly	Tyr	Arg	Val	Gly	Ser	Ser	Leu	Arg	Val	
		435					440					445				
TTT	GAT	CAT	GGC	ATG	TTT	TCG	GTG	GTG	TAT	AAT	TCT	TCA	GTT	ACA	TTC	1152
Phe	Asp	His	Gly	Met	Phe	Ser	Val	Val	Tyr	Asn	Ser	Ser	Val	Thr	Phe	
	450					455					460					
AAT	ATG	AAA	GGC	GCT	CTA	GTG	GCT	ATC	ACC	GAG	CTT	GGC	CCT	TCT	TTA	1200
Asn	Met	Lys	Gly	Ala	Leu	Val	Ala	Ile	Thr	Glu	Leu	Gly	Pro	Ser	Leu	
	465				470					475					480	
GGG	AGC	GTT	TTG	ACT	AAA	GGC	AGC	TTG	AAT	ATC	AAT	GTT	TCA	CTC	CCC	1248
Gly	Ser	Val	Leu	Thr	Lys	Gly	Ser	Leu	Asn	Ile	Asn	Val	Ser	Leu	Pro	
				485					490					495		
CAA	ACC	CTA	AGC	CTA	GCC	TAC	GCC	CAC	CAA	TTT	TTT	AAA	GAC	CAT	TTA	1296
Gln	Thr	Leu	Ser	Leu	Ala	Tyr	Ala	His	Gln	Phe	Phe	Lys	Asp	His	Leu	
			500					505					510			
AGA	ATA	GAG	GGG	GTG	TTT	GAG	CGT	ACC	TTT	TGG	AGT	CAA	GGG	AAT	AAA	1344
Arg	Ile	Glu	Gly	Val	Phe	Glu	Arg	Thr	Phe	Trp	Ser	Gln	Gly	Asn	Lys	
		515					520					525				
TTT	TTA	GTA	ACC	CCT	GAT	TTT	GCG	AAC	GCT	ACT	TAC	AAG	GGC	TTG	AGC	1392
Phe	Leu	Val	Thr	Pro	Asp	Phe	Ala	Asn	Ala	Thr	Tyr	Lys	Gly	Leu	Ser	
	530					535					540					
GGA	ACG	GTG	GCT	TCA	CTA	GAC	TCT	GAG	ACG	CTT	AAA	AAA	ATG	GTA	GGC	1440
Gly	Thr	Val	Ala	Ser	Leu	Asp	Ser	Glu	Thr	Leu	Lys	Lys	Met	Val	Gly	
	545				550					555				560		
TTA	GCG	AAT	TTT	AAA	AGC	GTG	ATG	AAC	ATG	GGG	GCT	GGC	TGG	AGA	GAC	1488
Leu	Ala	Asn	Phe	Lys	Ser	Val	Met	Asn	Met	Gly	Ala	Gly	Trp	Arg	Asp	
				565				570						575		
ACC	AAC	ACC	TTT	AGA	TTA	GGG	GTA	ACT	TAC	ATG	GGT	AAA	AGC	TTG	CGT	1536
Thr	Asn	Thr	Phe	Arg	Leu	Gly	Val	Thr	Tyr	Met	Gly	Lys	Ser	Leu	Arg	
			580					585					590			

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TTG ATG GGT GCT ATT GAT TAT GAC CAA GCC CCA AGC CCC CAA GAC GCG 1584  
 Leu Met Gly Ala Ile Asp Tyr Asp Gln Ala Pro Ser Pro Gln Asp Ala  
           595                                600                                605

ATA GGT ATC CCA GAT TCC AAT GGC TAT ACC GTG GCT TTT GGG ACT AAA 1632  
 Ile Gly Ile Pro Asp Ser Asn Gly Tyr Thr Val Ala Phe Gly Thr Lys  
           610                                615                                620

TAC AAT TTT AGG GGC TTT GAT TTA GGC GTA GCG GGG AGT TTC ACT TTT 1680  
 Tyr Asn Phe Arg Gly Phe Asp Leu Gly Val Ala Gly Ser Phe Thr Phe  
           625                                630                                635                                640

AAA AGC AAC CGC TCC AGT TTG TAT CAA TCC CCA AAC ATT GGG CAA TTG 1728  
 Lys Ser Asn Arg Ser Ser Leu Tyr Gln Ser Pro Asn Ile Gly Gln Leu  
                                 645                                650                                655

AGA ATC TTT AGC GCC TCT TTA GGC TAT CGC TGG TAA 1764  
 Arg Ile Phe Ser Ala Ser Leu Gly Tyr Arg Trp \*  
                                 660                                665

## (2) INFORMATION FOR SEQ ID NO: 60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met Lys Asn Phe Ser Pro Leu Cys Cys Phe Lys Lys Leu Lys Lys Arg  
   1                                5                                10                                15

His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala Asn Gly Phe  
           20                                25                                30

Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly Ser Ala Tyr  
           35                                40                                45

Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn Pro Ala Asn  
           50                                55                                60

Met Gly Phe Thr Asn Asp Trp Asp Glu Asn Arg Ser Glu Phe Glu Met  
   65                                70                                75                                80

Thr Thr Thr Val Ile Asn Ile Pro Ala Phe Lys Phe Gln Val Pro Thr  
           85                                90                                95

Thr Asn Gln Gly Leu Tyr Ser Val Thr Ser Leu Gln Ile Asp Lys Ser  
           100                                105                                110

Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu Ser Asn Ile  
           115                                120                                125

Leu Lys Ala Leu Gly Asn Thr Ala Ala Thr Asn Gly Leu Ser Gln Ala  
           130                                135                                140

Ile Asn Arg Val Gln Gly Leu Met Asn Leu Thr Asn Gln Lys Val Val

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145		150		155		160
Thr Leu Ala Ser Lys Pro Asp Thr Gln Ile Val Asn Gly Trp Thr Gly						
		165		170		175
Thr Thr Asn Phe Val Leu Pro Lys Phe Phe Tyr Lys Thr Arg Thr His						
		180		185		190
Asn Gly Phe Thr Phe Gly Gly Ser Phe Thr Ala Pro Ser Gly Leu Gly						
		195		200		205
Met Lys Trp Asn Gly Lys Gly Gly Glu Phe Leu His Asp Val Phe Ile						
		210		215		220
Met Met Val Glu Leu Ala Pro Ser Met Ser Tyr Thr Val Asn Lys His						
		225		230		235
Phe Ser Val Gly Val Gly Leu Arg Gly Leu Tyr Ala Thr Gly Ser Phe						
		245		250		255
Asn Asn Thr Val Tyr Val Pro Leu Glu Gly Ala Ser Val Leu Ser Ala						
		260		265		270
Glu Gln Ile Leu Asn Leu Pro Asn Asn Val Phe Ala Asp Gln Val Pro						
		275		280		285
Ser Asn Met Met Thr Leu Leu Gly Asn Ile Gly Tyr Gln Pro Ala Leu						
		290		295		300
Asn Cys Gln Lys Ala Gly Gly Asp Met Ser Asp Gln Ser Cys Gln Glu						
		305		310		315
Phe Tyr Asn Gly Leu Lys Lys Ile Met Gly Tyr Ser Gly Leu Ile Lys						
		325		330		335
Ala Ser Ala Asn Leu Tyr Gly Thr Thr Gln Val Val Gln Lys Ser Asn						
		340		345		350
Gly Gln Gly Val Ser Gly Gly Tyr Arg Val Gly Ser Ser Leu Arg Val						
		355		360		365
Phe Asp His Gly Met Phe Ser Val Val Tyr Asn Ser Ser Val Thr Phe						
		370		375		380
Asn Met Lys Gly Ala Leu Val Ala Ile Thr Glu Leu Gly Pro Ser Leu						
		385		390		395
Gly Ser Val Leu Thr Lys Gly Ser Leu Asn Ile Asn Val Ser Leu Pro						
		405		410		415
Gln Thr Leu Ser Leu Ala Tyr Ala His Gln Phe Phe Lys Asp His Leu						
		420		425		430
Arg Ile Glu Gly Val Phe Glu Arg Thr Phe Trp Ser Gln Gly Asn Lys						
		435		440		445
Phe Leu Val Thr Pro Asp Phe Ala Asn Ala Thr Tyr Lys Gly Leu Ser						
		450		455		460

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Gly Thr Val Ala Ser Leu Asp Ser Glu Thr Leu Lys Lys Met Val Gly  
 465 470 475 480

Leu Ala Asn Phe Lys Ser Val Met Asn Met Gly Ala Gly Trp Arg Asp  
 485 490 495

Thr Asn Thr Phe Arg Leu Gly Val Thr Tyr Met Gly Lys Ser Leu Arg  
 500 505 510

Leu Met Gly Ala Ile Asp Tyr Asp Gln Ala Pro Ser Pro Gln Asp Ala  
 515 520 525

Ile Gly Ile Pro Asp Ser Asn Gly Tyr Thr Val Ala Phe Gly Thr Lys  
 530 535 540

Tyr Asn Phe Arg Gly Phe Asp Leu Gly Val Ala Gly Ser Phe Thr Phe  
 545 550 555 560

Lys Ser Asn Arg Ser Ser Leu Tyr Gln Ser Pro Asn Ile Gly Gln Leu  
 565 570 575

Arg Ile Phe Ser Ala Ser Leu Gly Tyr Arg Trp \*  
 580 585

## (2) INFORMATION FOR SEQ ID NO: 61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS190

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1443

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TTG GAA TTG AAA AAA ATC GCC CTT ATT TTA GAT GGC ATT GTA GCA AAA	48
Leu Glu Leu Lys Lys Ile Ala Leu Ile Leu Asp Gly Ile Val Ala Lys	
590 595 600	
AAT TTT TTA GAC TTG GTG CTA AGG CAT TAT TCT AAT CAT AAT TTT TAT	96
Asn Phe Leu Asp Leu Val Leu Arg His Tyr Ser Asn His Asn Phe Tyr	
605 610 615 620	
ATA GTG GTT GTC AAA AAT GAG AGC CTT ATC CCT AAA AAT TAC CCG AGC	144
Ile Val Val Val Lys Asn Glu Ser Leu Ile Pro Lys Asn Tyr Pro Ser	
625 630 635	
ACT TTC GCT TTT TAT TGT TTT GAT GCG ACT TCT AGT TTC AGG CTT TTG	192
Thr Phe Ala Phe Tyr Cys Phe Asp Ala Thr Ser Ser Phe Arg Leu Leu	
640 645 650	

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CAA	GTG	TTA	AAC	GAT	GAG	GTG	AGC	GAT	GCG	TTT	TTA	ATC	ATA	CAA	GAT	240
Gln	Val	Leu	Asn	Asp	Glu	Val	Ser	Asp	Ala	Phe	Leu	Ile	Ile	Gln	Asp	
		655					660					665				
TTT	AAA	GAA	CAG	CGC	ATC	ATT	CAT	AAA	ATC	ATT	CAA	ACC	CAT	TTC	AAA	288
Phe	Lys	Glu	Gln	Arg	Ile	Ile	His	Lys	Ile	Ile	Gln	Thr	His	Phe	Lys	
		670					675					680				
CGC	ATG	CGC	GTG	GTT	TTG	AGC	GTG	AAA	AAA	GAT	GGT	GAA	AAA	ACT	TTA	336
Arg	Met	Arg	Val	Val	Leu	Ser	Val	Lys	Lys	Asp	Gly	Glu	Lys	Thr	Leu	
		685					690				695				700	
GAA	AAT	AAT	GAA	GAA	AAT	AAA	GAT	GAA	AAG	CTT	ATT	TTG	ATT	GAT	GAA	384
Glu	Asn	Asn	Glu	Glu	Asn	Lys	Asp	Glu	Lys	Leu	Ile	Leu	Ile	Asp	Glu	
						705				710					715	
TTT	GAA	GTT	TTA	GCC	AAT	AAA	TTC	ATT	TCT	CGT	TTG	CCT	AAT	ATC	CCT	432
Phe	Glu	Val	Leu	Ala	Asn	Lys	Phe	Ile	Ser	Arg	Leu	Pro	Asn	Ile	Pro	
						720									730	
AGC	ACC	CCT	AGA	GAA	TTT	GGG	TTA	GCC	AAA	GGC	GAG	ATC	ATG	GAG	ATT	480
Ser	Thr	Pro	Arg	Glu	Phe	Gly	Leu	Ala	Lys	Gly	Glu	Ile	Met	Glu	Ile	
						735									745	
GAT	GTG	CCT	TTT	GGG	AGT	ATT	TTT	CCT	TAC	AGG	CAT	ATT	GGC	TCT	ATC	528
Asp	Val	Pro	Phe	Gly	Ser	Ile	Phe	Pro	Tyr	Arg	His	Ile	Gly	Ser	Ile	
						750									760	
AGC	CAA	CAA	GAA	TAC	AGG	ATT	GTA	GGG	CTT	TAT	CGC	AAC	GAT	GTT	TTG	576
Ser	Gln	Gln	Glu	Tyr	Arg	Ile	Val	Gly	Leu	Tyr	Arg	Asn	Asp	Val	Leu	
						765									780	
TTG	CTC	TCC	ACT	AAA	TCT	TTA	GTT	ATC	CAG	CCA	CGA	GAC	ATT	CTT	TTA	624
Leu	Leu	Ser	Thr	Lys	Ser	Leu	Val	Ile	Gln	Pro	Arg	Asp	Ile	Leu	Leu	
						785									795	
GTG	GCG	GGT	AAT	CCG	GAA	ATT	TTA	AAC	GCG	GTG	TAT	CTT	CAG	GTC	AAA	672
Val	Ala	Gly	Asn	Pro	Glu	Ile	Leu	Asn	Ala	Val	Tyr	Leu	Gln	Val	Lys	
						800									810	
AGC	AAT	GTC	GGG	CAG	TTC	CCA	GCC	CCC	TTT	GGT	AAG	AGC	ATT	TAT	TTA	720
Ser	Asn	Val	Gly	Gln	Phe	Pro	Ala	Pro	Phe	Gly	Lys	Ser	Ile	Tyr	Leu	
						815									825	
TAC	ATT	GAT	ATG	CGC	TTA	CCA	AAG	CCG	AAA	GCA	ATG	ATG	CCC	GAT	GTG	768
Tyr	Ile	Asp	Met	Arg	Leu	Pro	Lys	Pro	Lys	Ala	Met	Met	Pro	Asp	Val	
						830									840	
TAT	CAA	GCC	TTG	TTT	TTG	CAC	AAA	CAT	TTA	AAG	AGC	TAC	AAG	CTC	TAC	816
Tyr	Gln	Ala	Leu	Phe	Leu	His	Lys	His	Leu	Lys	Ser	Tyr	Lys	Leu	Tyr	
						845									860	
ATT	CAG	GTT	TTA	CAC	CCC	ACT	AGC	CCT	AAG	TTT	TGC	CAT	AAA	TTT	TTA	864
Ile	Gln	Val	Leu	His	Pro	Thr	Ser	Pro	Lys	Phe	Cys	His	Lys	Phe	Leu	
						865									875	
TCG	CTA	GAA	ACC	GAA	AGC	ATT	GAA	GTG	AAT	TTT	GAT	TTT	TAT	GGG	AAA	912
Ser	Leu	Glu	Thr	Glu	Ser	Ile	Glu	Val	Asn	Phe	Asp	Phe	Tyr	Gly	Lys	

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880	885	890	
AGT TTT ATC CAA AAA CTC CAT GAA GAC CAC CAG AAA AAA ATG GGT TTG			960
Ser Phe Ile Gln Lys Leu His Glu Asp His Gln Lys Lys Met Gly Leu			
895	900	905	
ATT GTG GTA GGC AGA GAG CTT TTT TTA TCT AAA AAA CAC CGA AAA GCC			1008
Ile Val Val Gly Arg Glu Leu Phe Leu Ser Lys Lys His Arg Lys Ala			
910	915	920	
CTA TAT AAA ACA GCC ACC CCG GTT TAT AAA ACC AAC ACT TCC GGC TTG			1056
Leu Tyr Lys Thr Ala Thr Pro Val Tyr Lys Thr Asn Thr Ser Gly Leu			
925	930	935	940
TCT AAA ACC TCT CAA AGC GTG GTG GTG TTG AAT GAA AGC TTG GAT ATC			1104
Ser Lys Thr Ser Gln Ser Val Val Val Leu Asn Glu Ser Leu Asp Ile			
945	950	955	
AAT GAG GAC ATG TCT TCA GTG ATC TTT GAT GTG TCT ATG CAA ATG GAT			1152
Asn Glu Asp Met Ser Ser Val Ile Phe Asp Val Ser Met Gln Met Asp			
960	965	970	
TTG GGC TTG TTG CTC TAT GAT TTT GAC CCT AAC AAG CGC TAT AAA AAC			1200
Leu Gly Leu Leu Leu Tyr Asp Phe Asp Pro Asn Lys Arg Tyr Lys Asn			
975	980	985	
GAG ATT GTC AAT CAT TAT GAA AAT TTA GCC AAC ACG CTC AAC CGC AAG			1248
Glu Ile Val Asn His Tyr Glu Asn Leu Ala Asn Thr Leu Asn Arg Lys			
990	995	1000	
ATT GAG ATT TTT CAA ACC GAT ATT AGA AAT CCT ATC ATG TAT CTC AAT			1296
Ile Glu Ile Phe Gln Thr Asp Ile Arg Asn Pro Ile Met Tyr Leu Asn			
1005	1010	1015	1020
TCT TTA AGA AAT CCC ATT TTG CAT TTC ATG CCT TTT GAA GAG TGC ATC			1344
Ser Leu Arg Asn Pro Ile Leu His Phe Met Pro Phe Glu Glu Cys Ile			
1025	1030	1035	
ACG CAC ACG CGC TTT TGG TGG TTT TTA TCC ACT AAA GTG GAA AAA TTA			1392
Thr His Thr Arg Phe Trp Trp Phe Leu Ser Thr Lys Val Glu Lys Leu			
1040	1045	1050	
GCG TTT TTA AAC GAT GAT AAC CCT CAA ATT TTT ATC CCT GTA GCG GAG			1440
Ala Phe Leu Asn Asp Asp Asn Pro Gln Ile Phe Ile Pro Val Ala Glu			
1055	1060	1065	
TGA			1443
*			

## (2) INFORMATION FOR SEQ ID NO: 62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Leu Glu Leu Lys Lys Ile Ala Leu Ile Leu Asp Gly Ile Val Ala Lys  
 1 5 10 15  
 Asn Phe Leu Asp Leu Val Leu Arg His Tyr Ser Asn His Asn Phe Tyr  
 20 25 30  
 Ile Val Val Val Lys Asn Glu Ser Leu Ile Pro Lys Asn Tyr Pro Ser  
 35 40 45  
 Thr Phe Ala Phe Tyr Cys Phe Asp Ala Thr Ser Ser Phe Arg Leu Leu  
 50 55 60  
 Gln Val Leu Asn Asp Glu Val Ser Asp Ala Phe Leu Ile Ile Gln Asp  
 65 70 75 80  
 Phe Lys Glu Gln Arg Ile Ile His Lys Ile Ile Gln Thr His Phe Lys  
 85 90 95  
 Arg Met Arg Val Val Leu Ser Val Lys Lys Asp Gly Glu Lys Thr Leu  
 100 105 110  
 Glu Asn Asn Glu Glu Asn Lys Asp Glu Lys Leu Ile Leu Ile Asp Glu  
 115 120 125  
 Phe Glu Val Leu Ala Asn Lys Phe Ile Ser Arg Leu Pro Asn Ile Pro  
 130 135 140  
 Ser Thr Pro Arg Glu Phe Gly Leu Ala Lys Gly Glu Ile Met Glu Ile  
 145 150 155 160  
 Asp Val Pro Phe Gly Ser Ile Phe Pro Tyr Arg His Ile Gly Ser Ile  
 165 170 175  
 Ser Gln Gln Glu Tyr Arg Ile Val Gly Leu Tyr Arg Asn Asp Val Leu  
 180 185 190  
 Leu Leu Ser Thr Lys Ser Leu Val Ile Gln Pro Arg Asp Ile Leu Leu  
 195 200 205  
 Val Ala Gly Asn Pro Glu Ile Leu Asn Ala Val Tyr Leu Gln Val Lys  
 210 215 220  
 Ser Asn Val Gly Gln Phe Pro Ala Pro Phe Gly Lys Ser Ile Tyr Leu  
 225 230 235 240  
 Tyr Ile Asp Met Arg Leu Pro Lys Pro Lys Ala Met Met Pro Asp Val  
 245 250 255  
 Tyr Gln Ala Leu Phe Leu His Lys His Leu Lys Ser Tyr Lys Leu Tyr  
 260 265 270  
 Ile Gln Val Leu His Pro Thr Ser Pro Lys Phe Cys His Lys Phe Leu  
 275 280 285  
 Ser Leu Glu Thr Glu Ser Ile Glu Val Asn Phe Asp Phe Tyr Gly Lys  
 290 295 300

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Ser Phe Ile Gln Lys Leu His Glu Asp His Gln Lys Lys Met Gly Leu  
 305 310 315 320  
 Ile Val Val Gly Arg Glu Leu Phe Leu Ser Lys Lys His Arg Lys Ala  
 325 330 335  
 Leu Tyr Lys Thr Ala Thr Pro Val Tyr Lys Thr Asn Thr Ser Gly Leu  
 340 345 350  
 Ser Lys Thr Ser Gln Ser Val Val Val Leu Asn Glu Ser Leu Asp Ile  
 355 360 365  
 Asn Glu Asp Met Ser Ser Val Ile Phe Asp Val Ser Met Gln Met Asp  
 370 375 380  
 Leu Gly Leu Leu Leu Tyr Asp Phe Asp Pro Asn Lys Arg Tyr Lys Asn  
 385 390 395 400  
 Glu Ile Val Asn His Tyr Glu Asn Leu Ala Asn Thr Leu Asn Arg Lys  
 405 410 415  
 Ile Glu Ile Phe Gln Thr Asp Ile Arg Asn Pro Ile Met Tyr Leu Asn  
 420 425 430  
 Ser Leu Arg Asn Pro Ile Leu His Phe Met Pro Phe Glu Glu Cys Ile  
 435 440 445  
 Thr His Thr Arg Phe Trp Trp Phe Leu Ser Thr Lys Val Glu Lys Leu  
 450 455 460  
 Ala Phe Leu Asn Asp Asp Asn Pro Gln Ile Phe Ile Pro Val Ala Glu  
 465 470 475 480

\*

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPC008 (HPC114, HPC145)

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ATG AAA AGC ATG CGT TTT AGC TAT ATT GAG CCA AGA GCG AAA TAC CTT  
 Met Lys Ser Met Arg Phe Ser Tyr Ile Glu Pro Arg Ala Lys Tyr Leu  
 485 490 495

ATC AGC AAG CTT TCT AAA ATT TGG GTT TTT TAC ATT TTT TTA TCT TTT 96  
 Ile Ser Lys Leu Ser Lys Ile Trp Val Phe Tyr Ile Phe Leu Ser Phe  
 500 505 510

GTG GTG ATA GGG GGG TTA GTG TGG TTT ATG CAC AAC GCC ATT AAA AGC 144  
 Val Val Ile Gly Gly Leu Val Trp Phe Met His Asn Ala Ile Lys Ser  
 515 520 525

ACT CAA GAC AAC GCG TCC AGT TTG ACG ATC CAA GAA AGG CTC TAC CGC 192  
 Thr Gln Asp Asn Ala Ser Ser Leu Thr Ile Gln Glu Arg Leu Tyr Arg  
 530 535 540 545

CAT GAA ATC ATC CGC TTA CAG GTT AAG ACT GAT GAA ACC TTA AAA CTC 240  
 His Glu Ile Ile Arg Leu Gln Val Lys Thr Asp Glu Thr Leu Lys Leu  
 550 555 560

ATT AAA GAA GCC AAA AAG CGT TTG AAT TAT AAC GAT GAT ATA CGA GAT 288  
 Ile Lys Glu Ala Lys Lys Arg Leu Asn Tyr Asn Asp Asp Ile Arg Asp  
 565 570 575

GTT TTG CAA GGG CTT TTG AAT ATT GTG CCG GAT TCC ATC ACT ATT AAT 336  
 Val Leu Gln Gly Leu Leu Asn Ile Val Pro Asp Ser Ile Thr Ile Asn  
 580 585 590

AGC ATT GAA ATA GAC CAG CAA AGC GTA GTG GTT AGT GGT AAA ACC CCT 384  
 Ser Ile Glu Ile Asp Gln Gln Ser Val Val Val Ser Gly Lys Thr Pro  
 595 600 605

TCT AAA GAA GCC TTT TAT TTT TTG TTT CAA AAC AAA CTA AAC CCC ATG 432  
 Ser Lys Glu Ala Phe Tyr Phe Leu Phe Gln Asn Lys Leu Asn Pro Met  
 610 615 620 625

TTT GAT TAT TCT AGG GCG GAA TTT TTC CCT TTA AGC GAC GGG TGG TTT 480  
 Phe Asp Tyr Ser Arg Ala Glu Phe Phe Pro Leu Ser Asp Gly Trp Phe  
 630 635 640

AAT TTT GTC TCC ACC AAC TTT TCT AAT TCC TTA CTG ATA AAA AAT CCG 528  
 Asn Phe Val Ser Thr Asn Phe Ser Asn Ser Leu Leu Ile Lys Asn Pro  
 645 650 655

GAG TCT ATT AAA TGA 543  
 Glu Ser Ile Lys \*  
 660

## (2) INFORMATION FOR SEQ ID NO: 64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Met Lys Ser Met Arg Phe Ser Tyr Ile Glu Pro Arg Ala Lys Tyr Leu  
 1 5 10 15

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Ile Ser Lys Leu Ser Lys Ile Trp Val Phe Tyr Ile Phe Leu Ser Phe  
                   20                  25                  30  
 Val Val Ile Gly Gly Leu Val Trp Phe Met His Asn Ala Ile Lys Ser  
                   35                  40                  45  
 Thr Gln Asp Asn Ala Ser Ser Leu Thr Ile Gln Glu Arg Leu Tyr Arg  
                   50                  55                  60  
 His Glu Ile Ile Arg Leu Gln Val Lys Thr Asp Glu Thr Leu Lys Leu  
                   65                  70                  75                  80  
 Ile Lys Glu Ala Lys Lys Arg Leu Asn Tyr Asn Asp Asp Ile Arg Asp  
                   85                  90                  95  
 Val Leu Gln Gly Leu Leu Asn Ile Val Pro Asp Ser Ile Thr Ile Asn  
                   100                  105                  110  
 Ser Ile Glu Ile Asp Gln Gln Ser Val Val Val Ser Gly Lys Thr Pro  
                   115                  120                  125  
 Ser Lys Glu Ala Phe Tyr Phe Leu Phe Gln Asn Lys Leu Asn Pro Met  
                   130                  135                  140  
 Phe Asp Tyr Ser Arg Ala Glu Phe Phe Pro Leu Ser Asp Gly Trp Phe  
                   145                  150                  155                  160  
 Asn Phe Val Ser Thr Asn Phe Ser Asn Ser Leu Leu Ile Lys Asn Pro  
                   165                  170                  175  
 Glu Ser Ile Lys \*  
                   180

## (2) INFORMATION FOR SEQ ID NO: 65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1746 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS013

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1746

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

ATG AAA AAA TTG GTT TTA GTC ATC TTT TTA ACG CTA GCG CTT TCA ATA                   48  
 Met Lys Lys Leu Val Leu Val Ile Phe Leu Thr Leu Ala Leu Ser Ile  
                   185                  190                  195  
 TCT GCA AAA GAA GTC AAA ATA GTG TTT TTA GAA ACT TCA GAC ATT CAT                   96  
 Ser Ala Lys Glu Val Lys Ile Val Phe Leu Glu Thr Ser Asp Ile His

200	205	210	
GGG CGG CTT TTT TCG TAT GAT TAT GCG ATT GGC GAG CAA AAA CCC AAT			144
Gly Arg Leu Phe Ser Tyr Asp Tyr Ala Ile Gly Glu Gln Lys Pro Asn			
215	220	225	
AAC GGC TTG ACA AGG ATT GCG ACT TTA ATC AAA AAG CAA AGG GCT GAG			192
Asn Gly Leu Thr Arg Ile Ala Thr Leu Ile Lys Lys Gln Arg Ala Glu			
230	235	240	245
AAT AAA AAT GTG GTT TTG ATT GAC AGC GGG GAT TTG TTG CAA GGC AAT			240
Asn Lys Asn Val Val Leu Ile Asp Ser Gly Asp Leu Leu Gln Gly Asn			
250	255	260	
AGC GCG GAG TTG TTT AAT GAT GAG CCA ATT CAT CCG CTA GTT AGA GCT			288
Ser Ala Glu Leu Phe Asn Asp Glu Pro Ile His Pro Leu Val Arg Ala			
265	270	275	
GAA AAC GAT TTG AAA TTT GAC ATT CGT GTG CTT GGC AAT CAC GAG TTT			336
Glu Asn Asp Leu Lys Phe Asp Ile Arg Val Leu Gly Asn His Glu Phe			
280	285	290	
AAT TTC AGT AAA GAT TTT TTA GAA AAG AAT ATT AAG GGG TTT AAT GGC			384
Asn Phe Ser Lys Asp Phe Leu Glu Lys Asn Ile Lys Gly Phe Asn Gly			
295	300	305	
GAT GTC ATG AAT GCG AAT ATC ATT AAA ATT GCG GAC AAT AAG CCG TTT			432
Asp Val Met Asn Ala Asn Ile Ile Lys Ile Ala Asp Asn Lys Pro Phe			
310	315	320	325
GTA AAA CCT TAT ATT ATT AAA AAA ATT GAT GGC GTG AGG GTG GCG GTT			480
Val Lys Pro Tyr Ile Ile Lys Lys Ile Asp Gly Val Arg Val Ala Val			
330	335	340	
GTG GGG TAT GTG GTG GCG CAC ATC CCA ACT TGG GAG GCC TCT ACG CCT			528
Val Gly Tyr Val Val Ala His Ile Pro Thr Trp Glu Ala Ser Thr Pro			
345	350	355	
GAA CAT TTT GCA GGA TTG AAG TTT TTG GAC GCT GAA GAA GCG TTA AAA			576
Glu His Phe Ala Gly Leu Lys Phe Leu Asp Ala Glu Glu Ala Leu Lys			
360	365	370	
AAG ACC TTA AAA GAG TTG AAA GGG AAG TAT GAT ATT TTG ATT GGC GCT			624
Lys Thr Leu Lys Glu Leu Lys Gly Lys Tyr Asp Ile Leu Ile Gly Ala			
375	380	385	
TTT CAT TTG GGG CGA GAA GAT GAG AAA GGT GGC GAC GGG ATA CCG GAT			672
Phe His Leu Gly Arg Glu Asp Glu Lys Gly Gly Asp Gly Ile Pro Asp			
390	395	400	405
TTA GCG AAA AAA TTC CCG CAA TTT GAC ATC ATT TTT GCA GGG CAT GAG			720
Leu Ala Lys Lys Phe Pro Gln Phe Asp Ile Ile Phe Ala Gly His Glu			
410	415	420	
CAT GCG GTT TAT AAC ACC AAA GTA GGG AAA GTG CAT ACC ATT GAG CCT			768
His Ala Val Tyr Asn Thr Lys Val Gly Lys Val His Thr Ile Glu Pro			
425	430	435	
GGA GCG TAT GGG GCT TAT CTG GCA AAG GGC GTG GTG GTA TTT GAC ACT			816

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Gly	Ala	Tyr	Gly	Ala	Tyr	Leu	Ala	Lys	Gly	Val	Val	Val	Phe	Asp	Thr	
	440						445					450				
AAA	ACG	AAG	AAA	AAA	ATT	ATA	ACG	ACT	GAA	AAT	TTA	CCC	ACA	AAA	GAT	864
Lys	Thr	Lys	Lys	Lys	Ile	Ile	Thr	Thr	Glu	Asn	Leu	Pro	Thr	Lys	Asp	
	455					460					465					
GTG	CCA	GAA	GAT	GAA	GAA	TTA	GCG	AAA	AAA	TAC	GAA	TAT	GTG	GAT	AAA	912
Val	Pro	Glu	Asp	Glu	Glu	Leu	Ala	Lys	Lys	Tyr	Glu	Tyr	Val	Asp	Lys	
470					475					480					485	
AAA	TCA	AAA	GAA	TAC	GCT	AAT	GAA	GTG	GTT	GGC	GAA	GTT	ACA	AAA	ACC	960
Lys	Ser	Lys	Glu	Tyr	Ala	Asn	Glu	Val	Val	Gly	Glu	Val	Thr	Lys	Thr	
				490					495					500		
TTT	ATT	GAC	AGG	CCT	GAT	TTT	ATC	ACA	GGA	GAA	GAA	AAA	ATC	ACC	ACG	1008
Phe	Ile	Asp	Arg	Pro	Asp	Phe	Ile	Thr	Gly	Glu	Glu	Lys	Ile	Thr	Thr	
			505					510					515			
ATG	CCC	ACC	GCC	GCC	TTG	CAA	GAA	ACA	CCG	GTG	ATA	GAA	TTG	ATT	AAT	1056
Met	Pro	Thr	Ala	Ala	Leu	Gln	Glu	Thr	Pro	Val	Ile	Glu	Leu	Ile	Asn	
	520						525					530				
AAA	GTG	CAA	AAA	TAT	TAC	GCA	AAA	GCC	GAT	GTT	TCA	GCG	GCA	GCC	TTA	1104
Lys	Val	Gln	Lys	Tyr	Tyr	Ala	Lys	Ala	Asp	Val	Ser	Ala	Ala	Ala	Leu	
	535					540					545					
TTC	AAT	TTT	GGG	GCG	AAT	TTG	AAA	AAA	GGG	CCT	TTC	AAA	AGA	AAA	GAT	1152
Phe	Asn	Phe	Gly	Ala	Asn	Leu	Lys	Lys	Gly	Pro	Phe	Lys	Arg	Lys	Asp	
550					555				560						565	
GTC	ACT	TAT	ATT	TAC	AAG	TTC	GCT	AAT	ACG	CTC	ATT	GGA	GTG	CGT	ATA	1200
Val	Thr	Tyr	Ile	Tyr	Lys	Phe	Ala	Asn	Thr	Leu	Ile	Gly	Val	Arg	Ile	
				570					575					580		
ACG	GGT	GAA	AAT	CTG	TTG	AAA	TAC	ATG	GAA	TGG	TCA	TAC	CGA	TTT	TAC	1248
Thr	Gly	Glu	Asn	Leu	Leu	Lys	Tyr	Met	Glu	Trp	Ser	Tyr	Arg	Phe	Tyr	
			585					590					595			
AAT	CAG	TTG	CAA	CCA	GGA	GAT	TTG	ACG	ATC	AGT	TTT	AAT	GAA	AAC	ATT	1296
Asn	Gln	Leu	Gln	Pro	Gly	Asp	Leu	Thr	Ile	Ser	Phe	Asn	Glu	Asn	Ile	
	600						605					610				
CGC	GGC	TAT	AAC	TTT	GAT	ATG	TTT	TCT	GGC	GTG	AAA	TAC	CAG	GTT	GAT	1344
Arg	Gly	Tyr	Asn	Phe	Asp	Met	Phe	Ser	Gly	Val	Lys	Tyr	Gln	Val	Asp	
	615					620					625					
GTT	ACA	AAA	CCC	GCC	GGA	CAA	AGG	ATT	ATC	AAT	CCG	ACA	ATC	AAC	AAC	1392
Val	Thr	Lys	Pro	Ala	Gly	Gln	Arg	Ile	Ile	Asn	Pro	Thr	Ile	Asn	Asn	
630					635					640					645	
AAA	CCC	ATT	GAC	CCC	AAA	GCC	ATC	TAT	AAA	TTA	GCG	ATC	AAC	AAT	TAC	1440
Lys	Pro	Ile	Asp	Pro	Lys	Ala	Ile	Tyr	Lys	Leu	Ala	Ile	Asn	Asn	Tyr	
				650					655					660		
CGA	TTC	GGA	ACA	TTA	TCC	ACG	ACA	TTG	AAT	TTG	GTT	ACA	GAC	GCT	GAT	1488
Arg	Phe	Gly	Thr	Leu	Ser	Thr	Thr	Leu	Asn	Leu	Val	Thr	Asp	Ala	Asp	
			665					670					675			

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AGG TAT TAT AAT TCT TAC GAT GAA CTG CAA GAT AAT GGG CAA ATA CGA 1536  
 Arg Tyr Tyr Asn Ser Tyr Asp Glu Leu Gln Asp Asn Gly Gln Ile Arg  
 680 685 690

GAT TTG ATC ATC AAA TAC ATC ACG GAA GAA AAA GGT GGG AAG GTA ACC 1584  
 Asp Leu Ile Ile Lys Tyr Ile Thr Glu Glu Lys Gly Gly Lys Val Thr  
 695 700 705

CCT GAA TTG GAG GGT AAT TGG GAA ATC ATC AAC TAC GAT TTC AAA AAC 1632  
 Pro Glu Leu Glu Gly Asn Trp Glu Ile Ile Asn Tyr Asp Phe Lys Asn  
 710 715 720 725

CCG TTG TTG GAA AAA TTG AGA GAA AAA TTA AAA GAG GGG AGC ATC AAA 1680  
 Pro Leu Leu Glu Lys Leu Arg Glu Lys Leu Lys Glu Gly Ser Ile Lys  
 730 735 740

ATC CCC ACC TCA AAG GAT GGG AGG ACT TTG AAT GTC AAA TCC ATT AAA 1728  
 Ile Pro Thr Ser Lys Asp Gly Arg Thr Leu Asn Val Lys Ser Ile Lys  
 745 750 755

GAG AGT GAA GTT AAA TAA 1746  
 Glu Ser Glu Val Lys \*  
 760

## (2) INFORMATION FOR SEQ ID NO: 66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Met Lys Lys Leu Val Leu Val Ile Phe Leu Thr Leu Ala Leu Ser Ile  
 1 5 10 15

Ser Ala Lys Glu Val Lys Ile Val Phe Leu Glu Thr Ser Asp Ile His  
 20 25 30

Gly Arg Leu Phe Ser Tyr Asp Tyr Ala Ile Gly Glu Gln Lys Pro Asn  
 35 40 45

Asn Gly Leu Thr Arg Ile Ala Thr Leu Ile Lys Lys Gln Arg Ala Glu  
 50 55 60

Asn Lys Asn Val Val Leu Ile Asp Ser Gly Asp Leu Leu Gln Gly Asn  
 65 70 75 80

Ser Ala Glu Leu Phe Asn Asp Glu Pro Ile His Pro Leu Val Arg Ala  
 85 90 95

Glu Asn Asp Leu Lys Phe Asp Ile Arg Val Leu Gly Asn His Glu Phe  
 100 105 110

Asn Phe Ser Lys Asp Phe Leu Glu Lys Asn Ile Lys Gly Phe Asn Gly  
 115 120 125

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Asp Val Met Asn Ala Asn Ile Ile Lys Ile Ala Asp Asn Lys Pro Phe  
 130 135 140  
 Val Lys Pro Tyr Ile Ile Lys Lys Ile Asp Gly Val Arg Val Ala Val  
 145 150 155 160  
 Val Gly Tyr Val Val Ala His Ile Pro Thr Trp Glu Ala Ser Thr Pro  
 165 170 175  
 Glu His Phe Ala Gly Leu Lys Phe Leu Asp Ala Glu Glu Ala Leu Lys  
 180 185 190  
 Lys Thr Leu Lys Glu Leu Lys Gly Lys Tyr Asp Ile Leu Ile Gly Ala  
 195 200 205  
 Phe His Leu Gly Arg Glu Asp Glu Lys Gly Gly Asp Gly Ile Pro Asp  
 210 215 220  
 Leu Ala Lys Lys Phe Pro Gln Phe Asp Ile Ile Phe Ala Gly His Glu  
 225 230 235 240  
 His Ala Val Tyr Asn Thr Lys Val Gly Lys Val His Thr Ile Glu Pro  
 245 250 255  
 Gly Ala Tyr Gly Ala Tyr Leu Ala Lys Gly Val Val Val Phe Asp Thr  
 260 265 270  
 Lys Thr Lys Lys Lys Ile Ile Thr Thr Glu Asn Leu Pro Thr Lys Asp  
 275 280 285  
 Val Pro Glu Asp Glu Glu Leu Ala Lys Lys Tyr Glu Tyr Val Asp Lys  
 290 295 300  
 Lys Ser Lys Glu Tyr Ala Asn Glu Val Val Gly Glu Val Thr Lys Thr  
 305 310 315 320  
 Phe Ile Asp Arg Pro Asp Phe Ile Thr Gly Glu Glu Lys Ile Thr Thr  
 325 330 335  
 Met Pro Thr Ala Ala Leu Gln Glu Thr Pro Val Ile Glu Leu Ile Asn  
 340 345 350  
 Lys Val Gln Lys Tyr Tyr Ala Lys Ala Asp Val Ser Ala Ala Ala Leu  
 355 360 365  
 Phe Asn Phe Gly Ala Asn Leu Lys Lys Gly Pro Phe Lys Arg Lys Asp  
 370 375 380  
 Val Thr Tyr Ile Tyr Lys Phe Ala Asn Thr Leu Ile Gly Val Arg Ile  
 385 390 395 400  
 Thr Gly Glu Asn Leu Leu Lys Tyr Met Glu Trp Ser Tyr Arg Phe Tyr  
 405 410 415  
 Asn Gln Leu Gln Pro Gly Asp Leu Thr Ile Ser Phe Asn Glu Asn Ile  
 420 425 430  
 Arg Gly Tyr Asn Phe Asp Met Phe Ser Gly Val Lys Tyr Gln Val Asp  
 435 440 445

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Val Thr Lys Pro Ala Gly Gln Arg Ile Ile Asn Pro Thr Ile Asn Asn  
 450 455 460

Lys Pro Ile Asp Pro Lys Ala Ile Tyr Lys Leu Ala Ile Asn Asn Tyr  
 465 470 475 480

Arg Phe Gly Thr Leu Ser Thr Thr Leu Asn Leu Val Thr Asp Ala Asp  
 485 490 495

Arg Tyr Tyr Asn Ser Tyr Asp Glu Leu Gln Asp Asn Gly Gln Ile Arg  
 500 505 510

Asp Leu Ile Ile Lys Tyr Ile Thr Glu Glu Lys Gly Gly Lys Val Thr  
 515 520 525

Pro Glu Leu Glu Gly Asn Trp Glu Ile Ile Asn Tyr Asp Phe Lys Asn  
 530 535 540

Pro Leu Leu Glu Lys Leu Arg Glu Lys Leu Lys Glu Gly Ser Ile Lys  
 545 550 555 560

Ile Pro Thr Ser Lys Asp Gly Arg Thr Leu Asn Val Lys Ser Ile Lys  
 565 570 575

Glu Ser Glu Val Lys \*  
 580

## (2) INFORMATION FOR SEQ ID NO: 67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1698 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS024 (HPS025)

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1698

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

ATG	ATG	TTT	TCT	TCA	ATG	TTT	GCT	TCG	TTG	GGG	ACT	CGT	ATC	ATG	CTG	48
Met	Met	Phe	Ser	Ser	Met	Phe	Ala	Ser	Leu	Gly	Thr	Arg	Ile	Met	Leu	
		585					590					595				
GTC	GTG	TTA	GCC	GCT	CTT	TTA	GGT	TTA	GGG	GGG	CTT	TTT	ATT	GGT	TTT	96
Val	Val	Leu	Ala	Ala	Leu	Leu	Gly	Leu	Gly	Gly	Leu	Phe	Ile	Gly	Phe	
		600				605					610					
GTA	AAG	GTT	ATG	CAA	AAA	GAT	GTG	TTA	GCG	CAA	CTC	ATG	GAG	CAT	TTA	144
Val	Lys	Val	Met	Gln	Lys	Asp	Val	Leu	Ala	Gln	Leu	Met	Glu	His	Leu	
615					620					625					630	

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GAA ACC GGG CAA TAC AAA AAG CGT GAA AAA ACG CTC GCT TAC ATG ACA	192
Glu Thr Gly Gln Tyr Lys Lys Arg Glu Lys Thr Leu Ala Tyr Met Thr	
635 640 645	
AAA ATT ATT GAA CAG GGC ATT CAT GAG TAT TAC AAA AAT TTT GAC AAT	240
Lys Ile Ile Glu Gln Gly Ile His Glu Tyr Tyr Lys Asn Phe Asp Asn	
650 655 660	
GCT ACT GCA AGA AAA ATG GCG TTA GAT TAT TTC AAA CGC ATC AAC GAC	288
Ala Thr Ala Arg Lys Met Ala Leu Asp Tyr Phe Lys Arg Ile Asn Asp	
665 670 675	
GAT AAG GGC ATG ATT TAT ATG GTG GTG GTG GAT AAA AAC GGG GTG GTA	336
Asp Lys Gly Met Ile Tyr Met Val Val Val Asp Lys Asn Gly Val Val	
680 685 690	
TTG TTT GAT CCG GTC AAT CCT AAA ACC GTA GGC CAA TCA GGG CTT GAC	384
Leu Phe Asp Pro Val Asn Pro Lys Thr Val Gly Gln Ser Gly Leu Asp	
695 700 705 710	
GCT CAG AGC GTT GAT GGG GTG TAT TAT GTT AGG GGG TAT TTG GAG GCG	432
Ala Gln Ser Val Asp Gly Val Tyr Tyr Val Arg Gly Tyr Leu Glu Ala	
715 720 725	
GCC AAA AAA GGG GGA GGC TAC ACT TAT TAT AAA ATG CCT AAA TAC GAT	480
Ala Lys Lys Gly Gly Gly Tyr Thr Tyr Lys Met Pro Lys Tyr Asp	
730 735 740	
GGA GGC GTA CCG GAG AAA AAA TTC GCC TAC TCG CAT TAT GAT GAA GTT	528
Gly Gly Val Pro Glu Lys Lys Phe Ala Tyr Ser His Tyr Asp Glu Val	
745 750 755	
TCT CAA ATG GTG ATC GCA ACG ACT TCC TAT TAC ACT GAC ATT AAC ACA	576
Ser Gln Met Val Ile Ala Thr Thr Ser Tyr Tyr Thr Asp Ile Asn Thr	
760 765 770	
GAA AAT AAA GCG ATC AAA GAA GGC GTG AAT AAG GTT TTT GAT GAA AAC	624
Glu Asn Lys Ala Ile Lys Glu Gly Val Asn Lys Val Phe Asp Glu Asn	
775 780 785 790	
ACC ACG AAA TTA TTC CTT TGG ATA CTG ACA GCG ACG ATA GCG CTA GTG	672
Thr Thr Lys Leu Phe Leu Trp Ile Leu Thr Ala Thr Ile Ala Leu Val	
795 800 805	
GTT TTG ACG CTC ATA TAC GCT AAA TTA AGG ATC GTG AAA CGC ATT GAT	720
Val Leu Thr Leu Ile Tyr Ala Lys Leu Arg Ile Val Lys Arg Ile Asp	
810 815 820	
GAA CTG GTC CTT AAA ATC AAC GCT TTT AGC CGT GGG GAT AAG GAT TTG	768
Glu Leu Val Leu Lys Ile Asn Ala Phe Ser Arg Gly Asp Lys Asp Leu	
825 830 835	
AGA GCC AAA ATT GAT GTG GGT GAT CGC AAC GAT GAA ATC TCG CAA GTG	816
Arg Ala Lys Ile Asp Val Gly Asp Arg Asn Asp Glu Ile Ser Gln Val	
840 845 850	
GGC CGT GGG ATC AAT TTG TTT GTG GAA AAC GCC CGC TTG ATT ATG GAA	864
Gly Arg Gly Ile Asn Leu Phe Val Glu Asn Ala Arg Leu Ile Met Glu	

855	860	865	870	
GAG ATT AAA GGG ATT TCC ACC CTC AAT AAA ACT TCA ATG GAT AAA TTA				912
Glu Ile Lys Gly Ile Ser Thr Leu Asn Lys Thr Ser Met Asp Lys Leu	875	880	885	
GTC CAA ATC ACG CAA GAA ACC CAA AAG AGC ATG AAA GAT TCC TCA ACC				960
Val Gln Ile Thr Gln Glu Thr Gln Lys Ser Met Lys Asp Ser Ser Thr	890	895	900	
ACC CTA AAT TCC GTG AAA AAT AAA GCC ACT GAT ATA GCG AGC ATG ATG				1008
Thr Leu Asn Ser Val Lys Asn Lys Ala Thr Asp Ile Ala Ser Met Met	905	910	915	
AAT GCT TCC ATA GAG CAA TCT CAA GGG TTA AGG AAG CGT TTG ATT GAA				1056
Asn Ala Ser Ile Glu Gln Ser Gln Gly Leu Arg Lys Arg Leu Ile Glu	920	925	930	
ACG CAA GGG CTG GTC AAA GAG AGC AAG GAT GCG ATC GGG GAT TTA TTT				1104
Thr Gln Gly Leu Val Lys Glu Ser Lys Asp Ala Ile Gly Asp Leu Phe	935	940	945	950
TCT CAA ATC ACA GAG AGC GCG CAC ACT GAA GAG GAA CTC TCT AGC AAA				1152
Ser Gln Ile Thr Glu Ser Ala His Thr Glu Glu Glu Leu Ser Ser Lys	955	960	965	
GTG GAG CAG CTA AGC CGT AAC GCT GAT GAT GTC AAA TCC ATT CTG GAT				1200
Val Glu Gln Leu Ser Arg Asn Ala Asp Asp Val Lys Ser Ile Leu Asp	970	975	980	
ATT ATC AAT GAT ATT GCC GAT CAA ACG AAT TTA TTA GCC CTA AAC GCT				1248
Ile Ile Asn Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala	985	990	995	
GCT ATT GAA GCC GCA AGG GCT GGC GAG CAT GGC AGA GGC TTT GCG GTG				1296
Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala Val	1000	1005	1010	
GTG GCT GAT GAA GTT AGG AAT TTA GCC GGG CGC ACT CAA AAG TCT TTA				1344
Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser Leu	1015	1020	1025	1030
GCC GAA ATC AAT TCC ACT ATC ATG GTG ATT GTC CAA GAA ATC AAT GCC				1392
Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn Ala	1035	1040	1045	
GTG AGT TCG CAA ATG AAT CTC AAT TCG CAA AAA ATG GAG CGT TTG AGC				1440
Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu Ser	1050	1055	1060	
GAT ATG AGT AAA AGC GTG CAA GAA ACT TAC GAA AAA ATG AGT TCT AAT				1488
Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser Asn	1065	1070	1075	
TTA AGC TCA GTC GTG TCA GAC AGC AAT CAA AGC ATG GAC GAT TAC GCC				1536
Leu Ser Ser Val Val Ser Asp Ser Asn Gln Ser Met Asp Asp Tyr Ala	1080	1085	1090	
AAA TCC GGA CAC CAA ATT GAA GTT ATG GTA AGC GAT TTT GCA GAG GTG				1584

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Lys Ser Gly His Gln Ile Glu Val Met Val Ser Asp Phe Ala Glu Val  
 1095 1100 1105 1110

GAA AAA GTG GCT TCT AAG ACT TTA GCG GAT TCT TCA GAT ATT TTA AAC 1632  
 Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu Asn  
 1115 1120 1125

ATC GCT ACG CAT GTG AGT GGA ACG ACC ATG AAT TTA GAC AAA CAA GTG 1680  
 Ile Ala Thr His Val Ser Gly Thr Met Asn Leu Asp Lys Gln Val  
 1130 1135 1140

AAT TTG TTT AAA ACT TAA 1698  
 Asn Leu Phe Lys Thr \*  
 1145

## (2) INFORMATION FOR SEQ ID NO: 68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Met Met Phe Ser Ser Met Phe Ala Ser Leu Gly Thr Arg Ile Met Leu  
 1 5 10 15

Val Val Leu Ala Ala Leu Leu Gly Leu Gly Gly Leu Phe Ile Gly Phe  
 20 25 30

Val Lys Val Met Gln Lys Asp Val Leu Ala Gln Leu Met Glu His Leu  
 35 40 45

Glu Thr Gly Gln Tyr Lys Lys Arg Glu Lys Thr Leu Ala Tyr Met Thr  
 50 55 60

Lys Ile Ile Glu Gln Gly Ile His Glu Tyr Tyr Lys Asn Phe Asp Asn  
 65 70 75 80

Ala Thr Ala Arg Lys Met Ala Leu Asp Tyr Phe Lys Arg Ile Asn Asp  
 85 90 95

Asp Lys Gly Met Ile Tyr Met Val Val Val Asp Lys Asn Gly Val Val  
 100 105 110

Leu Phe Asp Pro Val Asn Pro Lys Thr Val Gly Gln Ser Gly Leu Asp  
 115 120 125

Ala Gln Ser Val Asp Gly Val Tyr Tyr Val Arg Gly Tyr Leu Glu Ala  
 130 135 140

Ala Lys Lys Gly Gly Gly Tyr Thr Tyr Tyr Lys Met Pro Lys Tyr Asp  
 145 150 155 160

Gly Gly Val Pro Glu Lys Lys Phe Ala Tyr Ser His Tyr Asp Glu Val  
 165 170 175

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Ser Gln Met Val Ile Ala Thr Thr Ser Tyr Tyr Thr Asp Ile Asn Thr  
 180 185 190  
 Glu Asn Lys Ala Ile Lys Glu Gly Val Asn Lys Val Phe Asp Glu Asn  
 195 200 205  
 Thr Thr Lys Leu Phe Leu Trp Ile Leu Thr Ala Thr Ile Ala Leu Val  
 210 215 220  
 Val Leu Thr Leu Ile Tyr Ala Lys Leu Arg Ile Val Lys Arg Ile Asp  
 225 230 235 240  
 Glu Leu Val Leu Lys Ile Asn Ala Phe Ser Arg Gly Asp Lys Asp Leu  
 245 250 255  
 Arg Ala Lys Ile Asp Val Gly Asp Arg Asn Asp Glu Ile Ser Gln Val  
 260 265 270  
 Gly Arg Gly Ile Asn Leu Phe Val Glu Asn Ala Arg Leu Ile Met Glu  
 275 280 285  
 Glu Ile Lys Gly Ile Ser Thr Leu Asn Lys Thr Ser Met Asp Lys Leu  
 290 295 300  
 Val Gln Ile Thr Gln Glu Thr Gln Lys Ser Met Lys Asp Ser Ser Thr  
 305 310 315 320  
 Thr Leu Asn Ser Val Lys Asn Lys Ala Thr Asp Ile Ala Ser Met Met  
 325 330 335  
 Asn Ala Ser Ile Glu Gln Ser Gln Gly Leu Arg Lys Arg Leu Ile Glu  
 340 345 350  
 Thr Gln Gly Leu Val Lys Glu Ser Lys Asp Ala Ile Gly Asp Leu Phe  
 355 360 365  
 Ser Gln Ile Thr Glu Ser Ala His Thr Glu Glu Glu Leu Ser Ser Lys  
 370 375 380  
 Val Glu Gln Leu Ser Arg Asn Ala Asp Asp Val Lys Ser Ile Leu Asp  
 385 390 395 400  
 Ile Ile Asn Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala  
 405 410 415  
 Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala Val  
 420 425 430  
 Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser Leu  
 435 440 445  
 Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn Ala  
 450 455 460  
 Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu Ser  
 465 470 475 480  
 Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser Asn  
 485 490 495

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Leu Ser Ser Val Val Ser Asp Ser Asn Gln Ser Met Asp Asp Tyr Ala  
500 505 510

Lys Ser Gly His Gln Ile Glu Val Met Val Ser Asp Phe Ala Glu Val  
515 520 525

Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu Asn  
530 535 540

Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Asp Lys Gln Val  
545 550 555 560

Asn Leu Phe Lys Thr \*  
565

## (2) INFORMATION FOR SEQ ID NO: 69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS036

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..855

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TTG GGT ATC AAT ATG TGT TCT AAA AAA ATA AGA AAT CTC ATT TTA TGC	48
Leu Gly Ile Asn Met Cys Ser Lys Lys Ile Arg Asn Leu Ile Leu Cys	
570 575 580	
TTT GGT TTT ATG TTG GGC TTG CAC GCT GAA GAA AAT ACG ACT GAA GGA	96
Phe Gly Phe Met Leu Gly Leu His Ala Glu Glu Asn Thr Thr Glu Gly	
585 590 595	
AAT ATG ACT GAA GAA AAT ATC TCT AAA GAC GCT CCC ATT CTT TTG GAA	144
Asn Met Thr Glu Glu Asn Ile Ser Lys Asp Ala Pro Ile Leu Leu Glu	
600 605 610	
GAA AAA CGC GCC CAA ACG CTA GAA TTT AAA GAA GAA AAG GAA GCT AAA	192
Glu Lys Arg Ala Gln Thr Leu Glu Phe Lys Glu Glu Lys Glu Ala Lys	
615 620 625 630	
AAG AAT ATT GAT GAA AAA AGC CTG CTT GAA GAA ATC CAT AAG AAA AAA	240
Lys Asn Ile Asp Glu Lys Ser Leu Leu Glu Glu Ile His Lys Lys Lys	
635 640 645	
CGC CAA CTT TAC ATG CTC AAA GGG GAA TTG CAT GAA AAA AAT GAA TCT	288
Arg Gln Leu Tyr Met Leu Lys Gly Glu Leu His Glu Lys Asn Glu Ser	
650 655 660	

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CTC TTG TTC CAA CGA ATG GCT AAA AAT AAG AGC GGT TTT TTT ATA GGC Leu Leu Phe Gln Arg Met Ala Lys Asn Lys Ser Gly Phe Phe Ile Gly 665 670 675	336
GTA ATC CTT GGC GAT ATA GGG GTT AGC GCT CAT TCT TAT GAG AAG TTT Val Ile Leu Gly Asp Ile Gly Val Ser Ala His Ser Tyr Glu Lys Phe 680 685 690	384
GAA CTT TTA AGC AAT ATT CAA GCT TCT CCT TTG TTG TAT GGC TTA AGG Glu Leu Leu Ser Asn Ile Gln Ala Ser Pro Leu Leu Tyr Gly Leu Arg 695 700 705 710	432
AGC GGG TAT CAA AAG TAT TTT GCT AAC GGG ATT AGC GCC TTA CGC TTT Ser Gly Tyr Gln Lys Tyr Phe Ala Asn Gly Ile Ser Ala Leu Arg Phe 715 720 725	480
TAT GGG GAG TAT TTA GGG GGG GCG ATG AAA GGA TTT AAA AGC GAT TCT Tyr Gly Glu Tyr Leu Gly Gly Ala Met Lys Gly Phe Lys Ser Asp Ser 730 735 740	528
TTA GCC TCT TAT CAA ACC GCA AGC TTG AAC ATT GAT TTG TTG ATG GAT Leu Ala Ser Tyr Gln Thr Ala Ser Leu Asn Ile Asp Leu Leu Met Asp 745 750 755	576
AAG CCT ATT GAC AAA GAA AAA AGG TTT GCG TTA GGG ATA TTT GGA GGC Lys Pro Ile Asp Lys Glu Lys Arg Phe Ala Leu Gly Ile Phe Gly Gly 760 765 770	624
GTT GGA GTG GGG TGG AAT GGG ATG TAT CAA AAT TTA AAA GAG GTT AAA Val Gly Val Gly Trp Asn Gly Met Tyr Gln Asn Leu Lys Glu Val Lys 775 780 785 790	672
GGG TAT TCA CAG CCT AAC GCT TTT GGA TTA GTG CTA AAT TTA GGG GTG Gly Tyr Ser Gln Pro Asn Ala Phe Gly Leu Val Leu Asn Leu Gly Val 795 800 805	720
AGC ATG ACG CTT AAC CTC AAA CAC CGC TTT GAA TTA GCC TTA AAA ATG Ser Met Thr Leu Asn Leu Lys His Arg Phe Glu Leu Ala Leu Lys Met 810 815 820	768
CCT CCC TTA AAA GAA ACT TCG CAA ACC TTT TTA TAT TAT TTT AAA AGC Pro Pro Leu Lys Glu Thr Ser Gln Thr Phe Leu Tyr Tyr Phe Lys Ser 825 830 835	816
ACT AAT ATT TAT TAT ATT AGT TAC AAC TAT TTA TTG TAA Thr Asn Ile Tyr Tyr Ile Ser Tyr Asn Tyr Leu Leu * 840 845 850	855

## (2) INFORMATION FOR SEQ ID NO: 70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Leu Gly Ile Asn Met Cys Ser Lys Lys Ile Arg Asn Leu Ile Leu Cys  
 1 5 10 15  
 Phe Gly Phe Met Leu Gly Leu His Ala Glu Glu Asn Thr Thr Glu Gly  
 20 25 30  
 Asn Met Thr Glu Glu Asn Ile Ser Lys Asp Ala Pro Ile Leu Leu Glu  
 35 40 45  
 Glu Lys Arg Ala Gln Thr Leu Glu Phe Lys Glu Glu Lys Glu Ala Lys  
 50 55 60  
 Lys Asn Ile Asp Glu Lys Ser Leu Leu Glu Glu Ile His Lys Lys Lys  
 65 70 75 80  
 Arg Gln Leu Tyr Met Leu Lys Gly Glu Leu His Glu Lys Asn Glu Ser  
 85 90 95  
 Leu Leu Phe Gln Arg Met Ala Lys Asn Lys Ser Gly Phe Phe Ile Gly  
 100 105 110  
 Val Ile Leu Gly Asp Ile Gly Val Ser Ala His Ser Tyr Glu Lys Phe  
 115 120 125  
 Glu Leu Leu Ser Asn Ile Gln Ala Ser Pro Leu Leu Tyr Gly Leu Arg  
 130 135 140  
 Ser Gly Tyr Gln Lys Tyr Phe Ala Asn Gly Ile Ser Ala Leu Arg Phe  
 145 150 155 160  
 Tyr Gly Glu Tyr Leu Gly Gly Ala Met Lys Gly Phe Lys Ser Asp Ser  
 165 170 175  
 Leu Ala Ser Tyr Gln Thr Ala Ser Leu Asn Ile Asp Leu Leu Met Asp  
 180 185 190  
 Lys Pro Ile Asp Lys Glu Lys Arg Phe Ala Leu Gly Ile Phe Gly Gly  
 195 200 205  
 Val Gly Val Gly Trp Asn Gly Met Tyr Gln Asn Leu Lys Glu Val Lys  
 210 215 220  
 Gly Tyr Ser Gln Pro Asn Ala Phe Gly Leu Val Leu Asn Leu Gly Val  
 225 230 235 240  
 Ser Met Thr Leu Asn Leu Lys His Arg Phe Glu Leu Ala Leu Lys Met  
 245 250 255  
 Pro Pro Leu Lys Glu Thr Ser Gln Thr Phe Leu Tyr Tyr Phe Lys Ser  
 260 265 270  
 Thr Asn Ile Tyr Tyr Ile Ser Tyr Asn Tyr Leu Leu \*  
 275 280 285

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 669 Base pairs

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(B) TYPE: Nucleotide  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS038

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) POSITION:1..669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATG GCT GAA AAT TCT TTC AAA AAT GTT TCC ACA CAA CCC AAA GTA TTT	48
Met Ala Glu Asn Ser Phe Lys Asn Val Ser Thr Gln Pro Lys Val Phe	
290 295 300	
TTC TTA TTG CCA GCT AAA ACC CTG TTT CTT TTA GGA GGC GTT TTT AGC	96
Phe Leu Leu Pro Ala Lys Thr Leu Phe Leu Leu Gly Gly Val Phe Ser	
305 310 315	
GCG TTT TTT ATC CTT ATT GCT GGC TTG GTT TTT TTT GAT TAT GCT CAT	144
Ala Phe Phe Ile Leu Ile Ala Gly Leu Val Phe Phe Asp Tyr Ala His	
320 325 330	
TTG ATG GAC AAT GCC ATT TTT AAT TTT GCG CGT TCA ACC CCC TTT AAT	192
Leu Met Asp Asn Ala Ile Phe Asn Phe Ala Arg Ser Thr Pro Phe Asn	
335 340 345	
TCC AGC CCT ATT TTA ACT CTA ATC CTC CAA AAT ATC GCT AAT TTA GGC	240
Ser Ser Pro Ile Leu Thr Leu Ile Leu Gln Asn Ile Ala Asn Leu Gly	
350 355 360 365	
TCT TCT CAA TTC GTG TTG CCT TTG AGT TTG TTG GTG GGG GTG TTT TTA	288
Ser Ser Gln Phe Val Leu Pro Leu Ser Leu Leu Val Gly Val Phe Leu	
370 375 380	
AGC CTT TAT CGC AGA AAC TTA GTG CTT GGG GTG TGG TTT GTG TTA AGC	336
Ser Leu Tyr Arg Arg Asn Leu Val Leu Gly Val Trp Phe Val Leu Ser	
385 390 395	
GTG ATC TTG TTT GAA GCC CTT TTA GAA TCT TTA AAA CAC CTT TTT GCA	384
Val Ile Leu Phe Glu Ala Leu Leu Glu Ser Leu Lys His Leu Phe Ala	
400 405 410	
TAT TCC ATT CAG TGG CTT TCG CGC AGC GCT AAT TTC CCT AAC GCT ACT	432
Tyr Ser Ile Gln Trp Leu Ser Arg Ser Ala Asn Phe Pro Asn Ala Thr	
415 420 425	
GCG CTT TCT TTA GTG CTA TTT TAT GGG TTG CTT ATT TTA TTG ATA CCC	480
Ala Leu Ser Leu Val Leu Phe Tyr Gly Leu Leu Ile Leu Leu Ile Pro	
430 435 440 445	
CAT TTA ATC ACG CAT CAA ACG CTT AAA AAT GTT CTT TTT TAT AGC TTA	528
His Leu Ile Thr His Gln Thr Leu Lys Asn Val Leu Phe Tyr Ser Leu	
450 455 460	

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TTT GGT TTG ATT TTT TTA ATA GGG TTA GCA CTG ATT GTT TTA GGG GTT	576
Phe Gly Leu Ile Phe Leu Ile Gly Leu Ala Leu Ile Val Leu Gly Val	
465 470 475	
TCT TTC AGT AGT GTT TTA GGA GGG TTT TGT TTA GGG GCG TTA GGG GCT	624
Ser Phe Ser Ser Val Leu Gly Gly Phe Cys Leu Gly Ala Leu Gly Ala	
480 485 490	
TGT TTT TCC ATA GGG ATT TAT TTG AGC GTG TTT CAA AAG ATC TAA	669
Cys Phe Ser Ile Gly Ile Tyr Leu Ser Val Phe Gln Lys Ile *	
495 500 505	

## (2) INFORMATION FOR SEQ ID NO: 72:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 Amino acids

(B) TYPE: Amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Met	Ala	Glu	Asn	Ser	Phe	Lys	Asn	Val	Ser	Thr	Gln	Pro	Lys	Val	Phe	1	5	10	15
Phe	Leu	Leu	Pro	Ala	Lys	Thr	Leu	Phe	Leu	Leu	Gly	Gly	Val	Phe	Ser	20	25	30	
Ala	Phe	Phe	Ile	Leu	Ile	Ala	Gly	Leu	Val	Phe	Phe	Asp	Tyr	Ala	His	35	40	45	
Leu	Met	Asp	Asn	Ala	Ile	Phe	Asn	Phe	Ala	Arg	Ser	Thr	Pro	Phe	Asn	50	55	60	
Ser	Ser	Pro	Ile	Leu	Thr	Leu	Ile	Leu	Gln	Asn	Ile	Ala	Asn	Leu	Gly	65	70	75	80
Ser	Ser	Gln	Phe	Val	Leu	Pro	Leu	Ser	Leu	Leu	Val	Gly	Val	Phe	Leu	85	90	95	
Ser	Leu	Tyr	Arg	Arg	Asn	Leu	Val	Leu	Gly	Val	Trp	Phe	Val	Leu	Ser	100	105	110	
Val	Ile	Leu	Phe	Glu	Ala	Leu	Leu	Glu	Ser	Leu	Lys	His	Leu	Phe	Ala	115	120	125	
Tyr	Ser	Ile	Gln	Trp	Leu	Ser	Arg	Ser	Ala	Asn	Phe	Pro	Asn	Ala	Thr	130	135	140	
Ala	Leu	Ser	Leu	Val	Leu	Phe	Tyr	Gly	Leu	Leu	Ile	Leu	Leu	Ile	Pro	145	150	155	160
His	Leu	Ile	Thr	His	Gln	Thr	Leu	Lys	Asn	Val	Leu	Phe	Tyr	Ser	Leu	165	170	175	
Phe	Gly	Leu	Ile	Phe	Leu	Ile	Gly	Leu	Ala	Leu	Ile	Val	Leu	Gly	Val	180	185	190	

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Ser Phe Ser Ser Val Leu Gly Gly Phe Cys Leu Gly Ala Leu Gly Ala  
 195 200 205

Cys Phe Ser Ile Gly Ile Tyr Leu Ser Val Phe Gln Lys Ile \*  
 210 215 220

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS039 (HPS147)

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ATG TCA GAA AAA GAA AGA CTG AAT GAA GTG ATC TTA GAA GAA GAA AAT	48
Met Ser Glu Lys Glu Arg Leu Asn Glu Val Ile Leu Glu Glu Glu Asn	
225 230 235	
AAT GGG AGC GGC ACT AAA AAG GTG TTT TTG ATC GTG GCT ATA GCC ATT	96
Asn Gly Ser Gly Thr Lys Lys Val Phe Leu Ile Val Ala Ile Ala Ile	
240 245 250 255	
ATC ATT TTA GCG GTG CTT TTA ATG GTG TTT TGG AAA AGC ACG AGA GTC	144
Ile Ile Leu Ala Val Leu Leu Met Val Phe Trp Lys Ser Thr Arg Val	
260 265 270	
GCT CCT AAA GAG ACT TTT TTA CAA ACC GAT AGC GGC ATG CAA AAA ATA	192
Ala Pro Lys Glu Thr Phe Leu Gln Thr Asp Ser Gly Met Gln Lys Ile	
275 280 285	
GGC AAC ACT AAA GAC GAG AAA AAA GAC GAT GAG TTT GAA AGC TTG AAT	240
Gly Asn Thr Lys Asp Glu Lys Lys Asp Asp Glu Phe Glu Ser Leu Asn	
290 295 300	
TTG GAT CCT TCC AAG CAA GAA GAC AAG CTA GAC AAA GTG GCG GAT AAT	288
Leu Asp Pro Ser Lys Gln Glu Asp Lys Leu Asp Lys Val Ala Asp Asn	
305 310 315	
GTT AAG AAG CAA GAA AAT GAT GCG TTT AAC ATG CCC ACT CAA ACC GAT	336
Val Lys Lys Gln Glu Asn Asp Ala Phe Asn Met Pro Thr Gln Thr Asp	
320 325 330 335	
CAA ACT CAA ACG GAG ATG AAA ACA ACA GAA GAA ACG CAA GAA GCT CAA	384
Gln Thr Gln Thr Glu Met Lys Thr Thr Glu Glu Thr Gln Glu Ala Gln	
340 345 350	

AAA GGA TTA AAA GTT GTT GAG CAC ACT AGC ACT CAA AAA GAA TCT CAA 432  
 Lys Gly Leu Lys Val Val Glu His Thr Ser Thr Gln Lys Glu Ser Gln  
 355 360 365

GCT GTG GCT AAA AAA GAA ATC TCC CAT AAA AAG CCT AAA GCA ACC CCT 480  
 Ala Val Ala Lys Lys Glu Ile Ser His Lys Lys Pro Lys Ala Thr Pro  
 370 375 380

AAA GAT AAG GAA GCC CAT AAA GAT AAA GAT AAG CAT GCG GTT AAA GAG 528  
 Lys Asp Lys Glu Ala His Lys Asp Lys Asp Lys His Ala Val Lys Glu  
 385 390 395

CTA AAA GTC AAA AAA GAA GCT CAT AAA GAA GTT CCT AAA AAA GCC AAT 576  
 Leu Lys Val Lys Lys Glu Ala His Lys Glu Val Pro Lys Lys Ala Asn  
 400 405 410 415

TCT AAA ACC ACT CTT ACT AAA GGG CAT TAT TTG CAA GTG GGG GTT TTT 624  
 Ser Lys Thr Thr Leu Thr Lys Gly His Tyr Leu Gln Val Gly Val Phe  
 420 425 430

GCG CAC ACG CCC AAT AAA GCC TTT TTG CAA GCG TTT AAC CAA TTC CCC 672  
 Ala His Thr Pro Asn Lys Ala Phe Leu Gln Ala Phe Asn Gln Phe Pro  
 435 440 445

CAT AAG ATT GAA GAT AGG GGG TCT ACT AAA CGC TAT CTC ATA GGC CCT 720  
 His Lys Ile Glu Asp Arg Gly Ser Thr Lys Arg Tyr Leu Ile Gly Pro  
 450 455 460

TAT AAG AAT AAG CAA GAA GCC TTA ATG CAT GCT GAT GAA GTC AGC AAA 768  
 Tyr Lys Asn Lys Gln Glu Ala Leu Met His Ala Asp Glu Val Ser Lys  
 465 470 475

AAG ATG ACT AAA CCG GTT GTC ATA GAA GCG CGG TAG 804  
 Lys Met Thr Lys Pro Val Val Ile Glu Ala Arg \*  
 480 485 490

## (2) INFORMATION FOR SEQ ID NO: 74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Met Ser Glu Lys Glu Arg Leu Asn Glu Val Ile Leu Glu Glu Glu Asn  
 1 5 10 15

Asn Gly Ser Gly Thr Lys Lys Val Phe Leu Ile Val Ala Ile Ala Ile  
 20 25 30

Ile Ile Leu Ala Val Leu Leu Met Val Phe Trp Lys Ser Thr Arg Val  
 35 40 45

Ala Pro Lys Glu Thr Phe Leu Gln Thr Asp Ser Gly Met Gln Lys Ile  
 50 55 60

Gly Asn Thr Lys Asp Glu Lys Lys Asp Asp Glu Phe Glu Ser Leu Asn  
 65 70 75 80  
 Leu Asp Pro Ser Lys Gln Glu Asp Lys Leu Asp Lys Val Ala Asp Asn  
 85 90 95  
 Val Lys Lys Gln Glu Asn Asp Ala Phe Asn Met Pro Thr Gln Thr Asp  
 100 105 110  
 Gln Thr Gln Thr Glu Met Lys Thr Thr Glu Glu Thr Gln Glu Ala Gln  
 115 120 125  
 Lys Gly Leu Lys Val Val Glu His Thr Ser Thr Gln Lys Glu Ser Gln  
 130 135 140  
 Ala Val Ala Lys Lys Glu Ile Ser His Lys Lys Pro Lys Ala Thr Pro  
 145 150 155 160  
 Lys Asp Lys Glu Ala His Lys Asp Lys Asp Lys His Ala Val Lys Glu  
 165 170 175  
 Leu Lys Val Lys Lys Glu Ala His Lys Glu Val Pro Lys Lys Ala Asn  
 180 185 190  
 Ser Lys Thr Thr Leu Thr Lys Gly His Tyr Leu Gln Val Gly Val Phe  
 195 200 205  
 Ala His Thr Pro Asn Lys Ala Phe Leu Gln Ala Phe Asn Gln Phe Pro  
 210 215 220  
 His Lys Ile Glu Asp Arg Gly Ser Thr Lys Arg Tyr Leu Ile Gly Pro  
 225 230 235 240  
 Tyr Lys Asn Lys Gln Glu Ala Leu Met His Ala Asp Glu Val Ser Lys  
 245 250 255  
 Lys Met Thr Lys Pro Val Val Ile Glu Ala Arg \*  
 260 265

## (2) INFORMATION FOR SEQ ID NO: 75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS040

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1545

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

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GTG AGG CAA GAA AAG TAT TTT CTG ACT TCT TCT TTA TCG CTT TTA TCG Val Arg Gln Glu Lys Tyr Phe Leu Thr Ser Ser Leu Ser Leu Leu Ser 270 275 280	48
TTT TTA TTA TGT CCT GCA GAA GCT TTT GAT TAT CGC TTT AGC GGT CGT Phe Leu Leu Cys Pro Ala Glu Ala Phe Asp Tyr Arg Phe Ser Gly Arg 285 290 295 300	96
GTG GAG AAC TTT TCT AAG ATT GGT TTT AAC AAT TCT CAA ATC AAT ACT Val Glu Asn Phe Ser Lys Ile Gly Phe Asn Asn Ser Gln Ile Asn Thr 305 310 315	144
AAA AAA GGG ATT TAT CCT ACT GAA AGT TTT ATA GAT ATT GTA ACT TTA Lys Lys Gly Ile Tyr Pro Thr Glu Ser Phe Ile Asp Ile Val Thr Leu 320 325 330	192
GCG CAA GTC AAA GTC AAT TTA CTC CCT AAA GGC ACC GAA AAC CAT AGG Ala Gln Val Lys Val Asn Leu Leu Pro Lys Gly Thr Glu Asn His Arg 335 340 345	240
CTC TCT GTC TCT TTG GGT GGG GCG ATT GCA GCC ATT CCT TAT GAT AAG Leu Ser Val Ser Leu Gly Gly Ala Ile Ala Ala Ile Pro Tyr Asp Lys 350 355 360	288
ACT AAA TAT GAT ATT AAC CAA GCT AAC GGG AAG ATT TTT GGC TCA ATT Thr Lys Tyr Asp Ile Asn Gln Ala Asn Gly Lys Ile Phe Gly Ser Ile 365 370 375 380	336
GTA GAG AAT TTC ATT GGG GGC TAT CAT GGA TAC TTT TTT AAT AAG TAT Val Glu Asn Phe Ile Gly Gly Tyr His Gly Tyr Phe Phe Asn Lys Tyr 385 390 395	384
CTT GGC CCT GCT TAT GCG GGG ACT TCT CAA TCA GCG AGC TAT CAT GCA Leu Gly Pro Ala Tyr Ala Gly Thr Ser Gln Ser Ala Ser Tyr His Ala 400 405 410	432
AGG CCT TAT GTG GTG GAT ACC GCT TTT TTA CGA TAC GAT TAC AAA GAT Arg Pro Tyr Val Val Asp Thr Ala Phe Leu Arg Tyr Asp Tyr Lys Asp 415 420 425	480
GTT TTT GGG TTT AAG GCG GGG CGC TAT GAA GCG AAT ATT GAT TTC ATG Val Phe Gly Phe Lys Ala Gly Arg Tyr Glu Ala Asn Ile Asp Phe Met 430 435 440	528
AGC GGA TCG AAT CAA GGG TGG GAA GTG TAT TAT CAG CCC TAT AAG ACT Ser Gly Ser Asn Gln Gly Trp Glu Val Tyr Tyr Gln Pro Tyr Lys Thr 445 450 455 460	576
GAA ACG CAA AGG TTA AGG TTT TGG TGG TGG AGT TCT TTT GGG AGA GGT Glu Thr Gln Arg Leu Arg Phe Trp Trp Trp Ser Phe Gly Arg Gly 465 470 475	624
TTA GCG TTC AAC TCT TGG ATT TAT GAG TTT TTT GCG ACG GTG CCT TAT Leu Ala Phe Asn Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro Tyr 480 485 490	672
TTG AAA AAG GGA GGC AAT CCT AAT AAC AGC AAC GAT TTC ATC AAT TAT Leu Lys Lys Gly Gly Asn Pro Asn Asn Ser Asn Asp Phe Ile Asn Tyr 495 500 505	720

GGC TGG CAT GGA ATC ACC ACA ACC TAT TCT TAT AAA GGT TTA GAC GCT Gly Trp His Gly Ile Thr Thr Thr Tyr Ser Tyr Lys Gly Leu Asp Ala 510 515 520	768
CAA TTT TTT TAT TAT TTT GCG CCT AAG ACT TAT AAC GCT CCT GGC TTT Gln Phe Phe Tyr Tyr Phe Ala Pro Lys Thr Tyr Asn Ala Pro Gly Phe 525 530 535 540	816
AAG CTG GTC TAT GAC ACG AAT AGG AAT TTT CAA AAT GTA GGC TTT CGC Lys Leu Val Tyr Asp Thr Asn Arg Asn Phe Gln Asn Val Gly Phe Arg 545 550 555	864
TCT CAA AGC ATG ATC ATG ACA ACC TTT CCT TTA TAC TAT AGA GGG TGG Ser Gln Ser Met Ile Met Thr Thr Phe Pro Leu Tyr Tyr Arg Gly Trp 560 565 570	912
TAT AAC CCA GAG ACA AAC ACT TAT AGT TTA GAA GAC AGC ACG CCT CAT Tyr Asn Pro Glu Thr Asn Thr Tyr Ser Leu Glu Asp Ser Thr Pro His 575 580 585	960
GGC TCG TTG TTG GGG AGG AAT GGC GTT ACT TTA AAT ATC CGC CAG GTT Gly Ser Leu Leu Gly Arg Asn Gly Val Thr Leu Asn Ile Arg Gln Val 590 595 600	1008
TTT TGG TGG GAT AAT TTC AAC TGG TCC ATT GGC TTT TAT AAC ACC TTT Phe Trp Trp Asp Asn Phe Asn Trp Ser Ile Gly Phe Tyr Asn Thr Phe 605 610 615 620	1056
GGC AAT TCG GAC GCT TTT TTA GGC TCT CAC ACG ATG CCA AGG GGT AAT Gly Asn Ser Asp Ala Phe Leu Gly Ser His Thr Met Pro Arg Gly Asn 625 630 635	1104
AAC ACT TCC TAT ATC GGT AGT GAA ATC TCC ATA ACG ACT AGG CAT GCC Asn Thr Ser Tyr Ile Gly Ser Glu Ile Ser Ile Thr Thr Arg His Ala 640 645 650	1152
GGA ATG ATT GGC TAT GAT TTT TGG GAT AAT ACG GCT TAT GAT GGG CTA Gly Met Ile Gly Tyr Asp Phe Thr Asp Asn Thr Ala Tyr Asp Gly Leu 655 660 665	1200
GCT GAT GCG ATC ACT AAC GCT AAC ACT TTC ACT TTT TAC ACT TCT GTT Ala Asp Ala Ile Thr Asn Ala Asn Thr Phe Thr Phe Tyr Thr Ser Val 670 675 680	1248
GGA GGG ATC CAT AAG CGT TTT GCA TGG CAT GTT TTT GGG CGC GTC TCT Gly Gly Ile His Lys Arg Phe Ala Trp His Val Phe Gly Arg Val Ser 685 690 695 700	1296
CAT GCG AAT AAA AAC GCG TTA GGG CAA GTG GGG AGG GCT AAT GAA TAT His Ala Asn Lys Asn Ala Leu Gly Gln Val Gly Arg Ala Asn Glu Tyr 705 710 715	1344
TCC TTG CAA TTC AAC GCG AGC TAT GCG TTC ACT GAA TCA ATC CTT CTT Ser Leu Gln Phe Asn Ala Ser Tyr Ala Phe Thr Glu Ser Ile Leu Leu 720 725 730	1392
AAC TTT AGG ATC ACT TAT TAT GGG GCT AGG ATC AAT AAA GGG TAT CAA Asn Phe Arg Ile Thr Tyr Tyr Gly Ala Arg Ile Asn Lys Gly Tyr Gln	1440

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735	740	745	
GCG GGG TAT TTT GGA GCG CCC AAA TTC AAT AAC CCT GAT GGC GAT TTT			1488
Ala Gly Tyr Phe Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp Phe			
750	755	760	
AGC GCT AAT TAC CAA GAC AGA AGT TAC ATG ATG ACC AAC CTC ACG CTG			1536
Ser Ala Asn Tyr Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr Leu			
765	770	775	780
AAG TTT TGA			1545
Lys Phe *			

## (2) INFORMATION FOR SEQ ID NO: 76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Val	Arg	Gln	Glu	Lys	Tyr	Phe	Leu	Thr	Ser	Ser	Leu	Ser	Leu	Leu	Ser
1				5					10					15	
Phe	Leu	Leu	Cys	Pro	Ala	Glu	Ala	Phe	Asp	Tyr	Arg	Phe	Ser	Gly	Arg
			20					25					30		
Val	Glu	Asn	Phe	Ser	Lys	Ile	Gly	Phe	Asn	Asn	Ser	Gln	Ile	Asn	Thr
	35						40					45			
Lys	Lys	Gly	Ile	Tyr	Pro	Thr	Glu	Ser	Phe	Ile	Asp	Ile	Val	Thr	Leu
	50					55					60				
Ala	Gln	Val	Lys	Val	Asn	Leu	Leu	Pro	Lys	Gly	Thr	Glu	Asn	His	Arg
65					70				75					80	
Leu	Ser	Val	Ser	Leu	Gly	Gly	Ala	Ile	Ala	Ala	Ile	Pro	Tyr	Asp	Lys
				85				90						95	
Thr	Lys	Tyr	Asp	Ile	Asn	Gln	Ala	Asn	Gly	Lys	Ile	Phe	Gly	Ser	Ile
	100							105					110		
Val	Glu	Asn	Phe	Ile	Gly	Gly	Tyr	His	Gly	Tyr	Phe	Phe	Asn	Lys	Tyr
	115						120					125			
Leu	Gly	Pro	Ala	Tyr	Ala	Gly	Thr	Ser	Gln	Ser	Ala	Ser	Tyr	His	Ala
	130					135					140				
Arg	Pro	Tyr	Val	Val	Asp	Thr	Ala	Phe	Leu	Arg	Tyr	Asp	Tyr	Lys	Asp
145					150					155				160	
Val	Phe	Gly	Phe	Lys	Ala	Gly	Arg	Tyr	Glu	Ala	Asn	Ile	Asp	Phe	Met
				165					170					175	
Ser	Gly	Ser	Asn	Gln	Gly	Trp	Glu	Val	Tyr	Tyr	Gln	Pro	Tyr	Lys	Thr

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180					185					190						
Glu	Thr	Gln	Arg	Leu	Arg	Phe	Trp	Trp	Trp	Ser	Ser	Phe	Gly	Arg	Gly	
195					200					205						
Leu	Ala	Phe	Asn	Ser	Trp	Ile	Tyr	Glu	Phe	Phe	Ala	Thr	Val	Pro	Tyr	
210					215					220						
Leu	Lys	Lys	Gly	Gly	Asn	Pro	Asn	Asn	Ser	Asn	Asp	Phe	Ile	Asn	Tyr	
225					230					235					240	
Gly	Trp	His	Gly	Ile	Thr	Thr	Thr	Tyr	Ser	Tyr	Lys	Gly	Leu	Asp	Ala	
245					250					255						
Gln	Phe	Phe	Tyr	Tyr	Phe	Ala	Pro	Lys	Thr	Tyr	Asn	Ala	Pro	Gly	Phe	
260					265					270						
Lys	Leu	Val	Tyr	Asp	Thr	Asn	Arg	Asn	Phe	Gln	Asn	Val	Gly	Phe	Arg	
275					280					285						
Ser	Gln	Ser	Met	Ile	Met	Thr	Thr	Phe	Pro	Leu	Tyr	Tyr	Arg	Gly	Trp	
290					295					300						
Tyr	Asn	Pro	Glu	Thr	Asn	Thr	Tyr	Ser	Leu	Glu	Asp	Ser	Thr	Pro	His	
305					310					315					320	
Gly	Ser	Leu	Leu	Gly	Arg	Asn	Gly	Val	Thr	Leu	Asn	Ile	Arg	Gln	Val	
325					330					335						
Phe	Trp	Trp	Asp	Asn	Phe	Asn	Trp	Ser	Ile	Gly	Phe	Tyr	Asn	Thr	Phe	
340					345					350						
Gly	Asn	Ser	Asp	Ala	Phe	Leu	Gly	Ser	His	Thr	Met	Pro	Arg	Gly	Asn	
355					360					365						
Asn	Thr	Ser	Tyr	Ile	Gly	Ser	Glu	Ile	Ser	Ile	Thr	Thr	Arg	His	Ala	
370					375					380						
Gly	Met	Ile	Gly	Tyr	Asp	Phe	Trp	Asp	Asn	Thr	Ala	Tyr	Asp	Gly	Leu	
385					390					395					400	
Ala	Asp	Ala	Ile	Thr	Asn	Ala	Asn	Thr	Phe	Thr	Phe	Tyr	Thr	Ser	Val	
405					410					415						
Gly	Gly	Ile	His	Lys	Arg	Phe	Ala	Trp	His	Val	Phe	Gly	Arg	Val	Ser	
420					425					430						
His	Ala	Asn	Lys	Asn	Ala	Leu	Gly	Gln	Val	Gly	Arg	Ala	Asn	Glu	Tyr	
435					440					445						
Ser	Leu	Gln	Phe	Asn	Ala	Ser	Tyr	Ala	Phe	Thr	Glu	Ser	Ile	Leu	Leu	
450					455					460						
Asn	Phe	Arg	Ile	Thr	Tyr	Tyr	Gly	Ala	Arg	Ile	Asn	Lys	Gly	Tyr	Gln	
465					470					475					480	
Ala	Gly	Tyr	Phe	Gly	Ala	Pro	Lys	Phe	Asn	Asn	Pro	Asp	Gly	Asp	Phe	
485					490					495						

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Ser Ala Asn Tyr Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr Leu  
 500 505 510

Lys Phe \*  
 515

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS048

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATG AAA AAG ATT ATT CTT GCA TGC CTT ATG GCT TTT GTG GGT GCC AAT	48
Met Lys Lys Ile Ile Leu Ala Cys Leu Met Ala Phe Val Gly Ala Asn	
520 525 530	
TTA AGC GCA GAG CCT AAG TGG TAT AGC AAG GCC TAC AAC AAA ACA AAC	96
Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn	
535 540 545	
ACC CAA AAA GGC TAT CTT TAT GGG AGT GGT TCA GCC ACT TCT AAA GAG	144
Thr Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu	
550 555 560	
GCT TCT AAA CAA AAA GCG TTA GCG GAT TTA GTG GCG TCT ATT AGC GTG	192
Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val	
565 570 575	
GTG GTT AAT TCC CAA ATC CAT ATT CAA AAA AGT CGT GTG GAC AAT AAG	240
Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys	
580 585 590 595	
TTA AAA TCC AGC GAT TCG CAA ACG ATT AAC TTA AAG ACC GAT GAC TTG	288
Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu	
600 605 610	
GAA TTG AAT AAT GTA GAA ATT GTC AAT CAA GAA GTG CAA AAA GGG ATC	336
Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Val Gln Lys Gly Ile	
615 620 625	
TAC TAC ACC AGA GTA AGG ATC AAT CAA AAC TTG TTT TTG CAG GGT TTA	384
Tyr Tyr Thr Arg Val Arg Ile Asn Gln Asn Leu Phe Leu Gln Gly Leu	
630 635 640	
AGG GAT AAG TAT AAC GCT CTT TAT GGG CAG TTT TCC ACC TTA ATG CCT	432

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Arg Asp Lys Tyr Asn Ala Leu Tyr Gly Gln Phe Ser Thr Leu Met Pro  
645 650 655

AAG GTT TGT AAA GGG GTT TTT TTA CAG CAA TCC AAG AGC ATG GGG GAT 480  
Lys Val Cys Lys Gly Val Phe Leu Gln Gln Ser Lys Ser Met Gly Asp  
660 665 670 675

TTA TTG GCT AAA GCG ATG CCT ATA GAA AGG ATT TTA AAA GCG TAT TCT 528  
Leu Leu Ala Lys Ala Met Pro Ile Glu Arg Ile Leu Lys Ala Tyr Ser  
680 685 690

GTT CCG GTG GGT TCG TTA GAA AAT TAT GAA AAA ATC TAT TAT CAA AAC 576  
Val Pro Val Gly Ser Leu Glu Asn Tyr Glu Lys Ile Tyr Tyr Gln Asn  
695 700 705

GCT TTC AAA CCT AAA GTG CAA ATC ACT TTT GAT AAC AAC GGC GAT GCG 624  
Ala Phe Lys Pro Lys Val Gln Ile Thr Phe Asp Asn Asn Gly Asp Ala  
710 715 720

GAA ATC AAA AGC GCT CTC ATA AGC GCT TAT GCC AGA GTG CTA ACC CCT 672  
Glu Ile Lys Ser Ala Leu Ile Ser Ala Tyr Ala Arg Val Leu Thr Pro  
725 730 735

AGT GAT GAA GAA AAA CTC TAT CAA ATC AAA AAT GAA GTT TTC ACA GAC 720  
Ser Asp Glu Glu Lys Leu Tyr Gln Ile Lys Asn Glu Val Phe Thr Asp  
740 745 750 755

AGT GCT AAT GGC ATC ACG CGC ATT AGA GTG GTT GTT AGC GCG AGC GAT 768  
Ser Ala Asn Gly Ile Thr Arg Ile Arg Val Val Val Ser Ala Ser Asp  
760 765 770

TGT CAA GGC ACG CCT GTA TTG AAT AGA AGC CTT GAA GTG GAT GAA AAG 816  
Cys Gln Gly Thr Pro Val Leu Asn Arg Ser Leu Glu Val Asp Glu Lys  
775 780 785

AAT AAG AAT TTT GCT ATC ACG CGC TTA CAA TCT TTG CTT TAT AAA GAA 864  
Asn Lys Asn Phe Ala Ile Thr Arg Leu Gln Ser Leu Leu Tyr Lys Glu  
790 795 800

CTG AAA GAT TAT GCC AAT AAA GAA GGG CAA GGC AAT ACG GGG TTA TAA 912  
Leu Lys Asp Tyr Ala Asn Lys Glu Gly Gln Gly Asn Thr Gly Leu \*  
805 810 815

## (2) INFORMATION FOR SEQ ID NO: 78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Met Lys Lys Ile Ile Leu Ala Cys Leu Met Ala Phe Val Gly Ala Asn  
1 5 10 15

Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn  
20 25 30

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Thr Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu  
 35 40 45  
 Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val  
 50 55 60  
 Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys  
 65 70 75 80  
 Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu  
 85 90 95  
 Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Val Gln Lys Gly Ile  
 100 105 110  
 Tyr Tyr Thr Arg Val Arg Ile Asn Gln Asn Leu Phe Leu Gln Gly Leu  
 115 120 125  
 Arg Asp Lys Tyr Asn Ala Leu Tyr Gly Gln Phe Ser Thr Leu Met Pro  
 130 135 140  
 Lys Val Cys Lys Gly Val Phe Leu Gln Gln Ser Lys Ser Met Gly Asp  
 145 150 155 160  
 Leu Leu Ala Lys Ala Met Pro Ile Glu Arg Ile Leu Lys Ala Tyr Ser  
 165 170 175  
 Val Pro Val Gly Ser Leu Glu Asn Tyr Glu Lys Ile Tyr Tyr Gln Asn  
 180 185 190  
 Ala Phe Lys Pro Lys Val Gln Ile Thr Phe Asp Asn Asn Gly Asp Ala  
 195 200 205  
 Glu Ile Lys Ser Ala Leu Ile Ser Ala Tyr Ala Arg Val Leu Thr Pro  
 210 215 220  
 Ser Asp Glu Glu Lys Leu Tyr Gln Ile Lys Asn Glu Val Phe Thr Asp  
 225 230 235 240  
 Ser Ala Asn Gly Ile Thr Arg Ile Arg Val Val Val Ser Ala Ser Asp  
 245 250 255  
 Cys Gln Gly Thr Pro Val Leu Asn Arg Ser Leu Glu Val Asp Glu Lys  
 260 265 270  
 Asn Lys Asn Phe Ala Ile Thr Arg Leu Gln Ser Leu Leu Tyr Lys Glu  
 275 280 285  
 Leu Lys Asp Tyr Ala Asn Lys Glu Gly Gln Gly Asn Thr Gly Leu \*  
 290 295 300

## (2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 834 Base pairs
  - (B) TYPE: Nucleotide
  - (C) STRANDEDNESS: both

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(D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS050

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) POSITION:1..834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

ATG AAA ACA AAC GGG CTT TTT AAA ATG TGG GGG CTG TTT TTA GTT TTA	48
Met Lys Thr Asn Gly Leu Phe Lys Met Trp Gly Leu Phe Leu Val Leu	
305 310 315 320	
ATC GCT TTA GTC TTT AAT GCA TGT TCT GAT AGC CAT AAA GAA AAA AAG	96
Ile Ala Leu Val Phe Asn Ala Cys Ser Asp Ser His Lys Glu Lys Lys	
325 330 335	
GAC GCT TTA GAA GTC ATT AAA CAA AGA GGG GTT TTA AAA GTG GGG GTT	144
Asp Ala Leu Glu Val Ile Lys Gln Arg Gly Val Leu Lys Val Gly Val	
340 345 350	
TTT AGC GAT AAG CCT CCT TTT GGC TCT GTG GAT TCT AAA GGG AAA TAT	192
Phe Ser Asp Lys Pro Pro Phe Gly Ser Val Asp Ser Lys Gly Lys Tyr	
355 360 365	
CAA GGC TAT GAT GTA GTT ATT GCT AAA CGC ATG GCT CTT GAT TTA TTG	240
Gln Gly Tyr Asp Val Val Ile Ala Lys Arg Met Ala Leu Asp Leu Leu	
370 375 380	
GGC GAT GAA AAT AAG ATT GAG TTT ATT CCT GTA GAA GCT TCA GCT AGG	288
Gly Asp Glu Asn Lys Ile Glu Phe Ile Pro Val Glu Ala Ser Ala Arg	
385 390 395 400	
GTG GAA TTT TTA AAA GCC AAT AAA GTG GAT ATT ATC ATG GCT AAT TTC	336
Val Glu Phe Leu Lys Ala Asn Lys Val Asp Ile Ile Met Ala Asn Phe	
405 410 415	
ACG CGC ACT AAA GAA AGA GAA AAA GTC GTG GAT TTC GCT AAG CCG TAT	384
Thr Arg Thr Lys Glu Arg Glu Lys Val Val Asp Phe Ala Lys Pro Tyr	
420 425 430	
ATG AAA GTC GCT TTA GGG GTG GTT TCT AAA GAT GGG GTC ATT AAA AAT	432
Met Lys Val Ala Leu Gly Val Val Ser Lys Asp Gly Val Ile Lys Asn	
435 440 445	
ATA GAA GAG TTG AAA GAT AAA GAG TTG ATT GTG AAT AAA GGC ACG ACA	480
Ile Glu Glu Leu Lys Asp Lys Glu Leu Ile Val Asn Lys Gly Thr Thr	
450 455 460	
GCG GAT TTT TAT TTC ACT AAA AAT TAC CCC AAT ATC AAG CTT TTG AAA	528
Ala Asp Phe Tyr Phe Thr Lys Asn Tyr Pro Asn Ile Lys Leu Leu Lys	
465 470 475 480	
TTT GAG CAA AAT ACA GAG ACT TTT TTA GCC CTT TTA AAC AAT AAG GCT	576

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Phe Glu Gln Asn Thr Glu Thr Phe Leu Ala Leu Leu Asn Asn Lys Ala  
485 490 495

ACC GCT CTA GCC CAT GAC AAC ACT TTA TTG CTC GCT TGG ACG AAA CAA 624  
Thr Ala Leu Ala His Asp Asn Thr Leu Leu Leu Ala Trp Thr Lys Gln  
500 505 510

CAC CCT GAA TTT AAA TTA GGC ATT ACA AGC CTT GGC GAT AAG GAT GTG 672  
His Pro Glu Phe Lys Leu Gly Ile Thr Ser Leu Gly Asp Lys Asp Val  
515 520 525

ATC GCT CCA GCG ATT AAA AAA GGC AAC CCC AAG CTT TTA GAA TGG TTG 720  
Ile Ala Pro Ala Ile Lys Lys Gly Asn Pro Lys Leu Leu Glu Trp Leu  
530 535 540

AAT AAC GAA ATA GAT TCC CTC ATT TCT AGC GAC TTC TTA AAA GAA GCT 768  
Asn Asn Glu Ile Asp Ser Leu Ile Ser Ser Asp Phe Leu Lys Glu Ala  
545 550 555 560

TAT CAA GAG ACT TTA GCA CCT GTT TAT GGC GAT GAA ATC AAA CCG GAA 816  
Tyr Gln Glu Thr Leu Ala Pro Val Tyr Gly Asp Glu Ile Lys Pro Glu  
565 570 575

GAA ATT ATT TTT GAA TGA 834  
Glu Ile Ile Phe Glu \*  
580

## (2) INFORMATION FOR SEQ ID NO: 80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 Amino acids  
(B) TYPE: Amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Met Lys Thr Asn Gly Leu Phe Lys Met Trp Gly Leu Phe Leu Val Leu  
1 5 10 15

Ile Ala Leu Val Phe Asn Ala Cys Ser Asp Ser His Lys Glu Lys Lys  
20 25 30

Asp Ala Leu Glu Val Ile Lys Gln Arg Gly Val Leu Lys Val Gly Val  
35 40 45

Phe Ser Asp Lys Pro Pro Phe Gly Ser Val Asp Ser Lys Gly Lys Tyr  
50 55 60

Gln Gly Tyr Asp Val Val Ile Ala Lys Arg Met Ala Leu Asp Leu Leu  
65 70 75 80

Gly Asp Glu Asn Lys Ile Glu Phe Ile Pro Val Glu Ala Ser Ala Arg  
85 90 95

Val Glu Phe Leu Lys Ala Asn Lys Val Asp Ile Ile Met Ala Asn Phe  
100 105 110

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Thr Arg Thr Lys Glu Arg Glu Lys Val Val Asp Phe Ala Lys Pro Tyr  
 115 120 125

Met Lys Val Ala Leu Gly Val Val Ser Lys Asp Gly Val Ile Lys Asn  
 130 135 140

Ile Glu Glu Leu Lys Asp Lys Glu Leu Ile Val Asn Lys Gly Thr Thr  
 145 150 155 160

Ala Asp Phe Tyr Phe Thr Lys Asn Tyr Pro Asn Ile Lys Leu Leu Lys  
 165 170 175

Phe Glu Gln Asn Thr Glu Thr Phe Leu Ala Leu Leu Asn Asn Lys Ala  
 180 185 190

Thr Ala Leu Ala His Asp Asn Thr Leu Leu Leu Ala Trp Thr Lys Gln  
 195 200 205

His Pro Glu Phe Lys Leu Gly Ile Thr Ser Leu Gly Asp Lys Asp Val  
 210 215 220

Ile Ala Pro Ala Ile Lys Lys Gly Asn Pro Lys Leu Leu Glu Trp Leu  
 225 230 235 240

Asn Asn Glu Ile Asp Ser Leu Ile Ser Ser Asp Phe Leu Lys Glu Ala  
 245 250 255

Tyr Gln Glu Thr Leu Ala Pro Val Tyr Gly Asp Glu Ile Lys Pro Glu  
 260 265 270

Glu Ile Ile Phe Glu \*  
 275

## (2) INFORMATION FOR SEQ ID NO: 81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS052

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1296

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GTG GCG TTA GCT GAA GAC GAT GGC TTT TAT ATG GGA GTG GGC TAT CAA	48
Val Ala Leu Ala Glu Asp Asp Gly Phe Tyr Met Gly Val Gly Tyr Gln	
280 285 290	
ATC GGC GGC GCG CAA CAA AAT ATC GAT AAC AAA GGC AGC ACC CTA AGG	96
Ile Gly Gly Ala Gln Gln Asn Ile Asp Asn Lys Gly Ser Thr Leu Arg	

295		300		305		310	
AAT AAT GTC ATT AAT AAT TTC CGC CAA GTG GGC GTG GGT ATG GCA GGG	144						
Asn Asn Val Ile Asn Asn Phe Arg Gln Val Gly Val Gly Met Ala Gly							
315		320		325			
GGT AAT GGG CTT TTA GCC TTA GCG ACA AAC ACG ACC ATG GAC GCT CTT	192						
Gly Asn Gly Leu Leu Ala Leu Ala Thr Asn Thr Thr Met Asp Ala Leu							
330		335		340			
TTA GGG ATA GGC AAC CAA ATT GTC AAT ACT AAT ACA ACT GTT AGC AAC	240						
Leu Gly Ile Gly Asn Gln Ile Val Asn Thr Asn Thr Thr Val Ser Asn							
345		350		355			
AAC AAC GCA GAA TTA ACC CAG TTT AAA AAA ATA CTC CCT CAA ATT GAG	288						
Asn Asn Ala Glu Leu Thr Gln Phe Lys Lys Ile Leu Pro Gln Ile Glu							
360		365		370			
CAA CGC TTT GAA ACG AAT AAA AAC GCT TAT AGC GTT CAA GCC TTG CAA	336						
Gln Arg Phe Glu Thr Asn Lys Asn Ala Tyr Ser Val Gln Ala Leu Gln							
375		380		385		390	
GTG TAT TTG AGT AAT GTG CTT TAT AAC TTG GTT AAT AAT AGT AAT AAT	384						
Val Tyr Leu Ser Asn Val Leu Tyr Asn Leu Val Asn Asn Ser Asn Asn							
395		400		405			
GGC AGT AAT AAT GGA GTC GTT CCT GAA TAT GTA GGA ATT ATA AAA GTT	432						
Gly Ser Asn Asn Gly Val Val Pro Glu Tyr Val Gly Ile Ile Lys Val							
410		415		420			
CTC TAT GGT TCT CAA AAT GAA TTC AGT CTC TTA GCC ACG GAG AGT GTG	480						
Leu Tyr Gly Ser Gln Asn Glu Phe Ser Leu Leu Ala Thr Glu Ser Val							
425		430		435			
GTG CTT TTA AAC GCG CTT ACA AGG GTG AAT CTG GAT AGT AAT TCG GTG	528						
Val Leu Leu Asn Ala Leu Thr Arg Val Asn Leu Asp Ser Asn Ser Val							
440		445		450			
TTT TTA AAA GGG CTA TTA GCC CAA ATG CAG CTT TTT AAT GAC ACT TCT	576						
Phe Leu Lys Gly Leu Leu Ala Gln Met Gln Leu Phe Asn Asp Thr Ser							
455		460		465		470	
TCA GCA AAG CTA GGC CAG ATC GCA GAA AAC TTG AAG AAC GGT GGT GCA	624						
Ser Ala Lys Leu Gly Gln Ile Ala Glu Asn Leu Lys Asn Gly Gly Ala							
475		480		485			
GGA TCA ATG CTC CAA AAG GAT GTG AAA ACC ATC TCG GAT CGA ATC GCT	672						
Gly Ser Met Leu Gln Lys Asp Val Lys Thr Ile Ser Asp Arg Ile Ala							
490		495		500			
ACT TAC CAA GAG AAT CTA AAA CAG CTA GGA GGG ATG CTA AAG AAT TAC	720						
Thr Tyr Gln Glu Asn Leu Lys Gln Leu Gly Gly Met Leu Lys Asn Tyr							
505		510		515			
GAT GAA CCC TAC TTG CCC CAA TTT GGG CCA GGC ACA AGC TCT CAG CAT	768						
Asp Glu Pro Tyr Leu Pro Gln Phe Gly Pro Gly Thr Ser Ser Gln His							
520		525		530			
GGG GTT ATT AAT GGC TTT GGC ATT CAA GTG GGC TAT AAG CAA TTT TTT	816						

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Gly Val Ile Asn Gly Phe Gly Ile Gln Val Gly Tyr Lys Gln Phe Phe  
 535 540 545 550  
 GGG AAC AAG CGG AAT ATA GGC TTA CGA TAT TAC GCT TTC TTT GAT TAT 864  
 Gly Asn Lys Arg Asn Ile Gly Leu Arg Tyr Tyr Ala Phe Phe Asp Tyr  
 555 560 565  
 GGC TTT ACG CAA TTG GGC AGT CTT AGC AGC GCC GTT AAA GCG AAT ATC 912  
 Gly Phe Thr Gln Leu Gly Ser Leu Ser Ser Ala Val Lys Ala Asn Ile  
 570 575 580  
 TTT ACT TAT GGC GCT GGC ACG GAC TTT TTA TGG AAT ATC TTT AGA AGG 960  
 Phe Thr Tyr Gly Ala Gly Thr Asp Phe Leu Trp Asn Ile Phe Arg Arg  
 585 590 595  
 GTT TTT AGC GAT CAG TCC TTG AAT GTG GGG GTG TTT GGG GGC ATT CAA 1008  
 Val Phe Ser Asp Gln Ser Leu Asn Val Gly Val Phe Gly Gly Ile Gln  
 600 605 610  
 ATA GCG GGT AAC ACT TGG GAT AGC TCT TTA AGA GGT CAA ATT GAA AAC 1056  
 Ile Ala Gly Asn Thr Trp Asp Ser Ser Leu Arg Gly Gln Ile Glu Asn  
 615 620 625 630  
 TCG TTT AAA GAA TAC CCC ACT CCC ACG AAT TTC CAA TTT TTG TTT AAT 1104  
 Ser Phe Lys Glu Tyr Pro Thr Pro Thr Asn Phe Gln Phe Leu Phe Asn  
 635 640 645  
 TTG GGT TTA AGG GCT CAT TTT GCC AGC ACC ATG CAC CGC CGG TTT TTG 1152  
 Leu Gly Leu Arg Ala His Phe Ala Ser Thr Met His Arg Arg Phe Leu  
 650 655 660  
 AGC GCG TCT CAA AGC ATT CAG CAT GGG ATG GAA TTT GGC GTG AAA ATC 1200  
 Ser Ala Ser Gln Ser Ile Gln His Gly Met Glu Phe Gly Val Lys Ile  
 665 670 675  
 CCG GCT ATC AAT CAA AGG TAT TTG AGG GCC AAT GGG GCT GAT GTG GAT 1248  
 Pro Ala Ile Asn Gln Arg Tyr Leu Arg Ala Asn Gly Ala Asp Val Asp  
 680 685 690  
 TAC AGG CGT TTG TAT GCG TTC TAT ATC AAT TAC ACG ATA GGT TTT TAA 1296  
 Tyr Arg Arg Leu Tyr Ala Phe Tyr Ile Asn Tyr Thr Ile Gly Phe \*  
 695 700 705 710

## (2) INFORMATION FOR SEQ ID NO: 82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Val Ala Leu Ala Glu Asp Asp Gly Phe Tyr Met Gly Val Gly Tyr Gln  
 1 5 10 15  
 Ile Gly Gly Ala Gln Gln Asn Ile Asp Asn Lys Gly Ser Thr Leu Arg  
 20 25 30

Asn Asn Val Ile Asn Asn Phe Arg Gln Val Gly Val Gly Met Ala Gly  
 35 40 45  
 Gly Asn Gly Leu Leu Ala Leu Ala Thr Asn Thr Thr Met Asp Ala Leu  
 50 55 60  
 Leu Gly Ile Gly Asn Gln Ile Val Asn Thr Asn Thr Thr Val Ser Asn  
 65 70 75 80  
 Asn Asn Ala Glu Leu Thr Gln Phe Lys Lys Ile Leu Pro Gln Ile Glu  
 85 90 95  
 Gln Arg Phe Glu Thr Asn Lys Asn Ala Tyr Ser Val Gln Ala Leu Gln  
 100 105 110  
 Val Tyr Leu Ser Asn Val Leu Tyr Asn Leu Val Asn Asn Ser Asn Asn  
 115 120 125  
 Gly Ser Asn Asn Gly Val Val Pro Glu Tyr Val Gly Ile Ile Lys Val  
 130 135 140  
 Leu Tyr Gly Ser Gln Asn Glu Phe Ser Leu Leu Ala Thr Glu Ser Val  
 145 150 155 160  
 Val Leu Leu Asn Ala Leu Thr Arg Val Asn Leu Asp Ser Asn Ser Val  
 165 170 175  
 Phe Leu Lys Gly Leu Leu Ala Gln Met Gln Leu Phe Asn Asp Thr Ser  
 180 185 190  
 Ser Ala Lys Leu Gly Gln Ile Ala Glu Asn Leu Lys Asn Gly Gly Ala  
 195 200 205  
 Gly Ser Met Leu Gln Lys Asp Val Lys Thr Ile Ser Asp Arg Ile Ala  
 210 215 220  
 Thr Tyr Gln Glu Asn Leu Lys Gln Leu Gly Gly Met Leu Lys Asn Tyr  
 225 230 235 240  
 Asp Glu Pro Tyr Leu Pro Gln Phe Gly Pro Gly Thr Ser Ser Gln His  
 245 250 255  
 Gly Val Ile Asn Gly Phe Gly Ile Gln Val Gly Tyr Lys Gln Phe Phe  
 260 265 270  
 Gly Asn Lys Arg Asn Ile Gly Leu Arg Tyr Tyr Ala Phe Phe Asp Tyr  
 275 280 285  
 Gly Phe Thr Gln Leu Gly Ser Leu Ser Ser Ala Val Lys Ala Asn Ile  
 290 295 300  
 Phe Thr Tyr Gly Ala Gly Thr Asp Phe Leu Trp Asn Ile Phe Arg Arg  
 305 310 315 320  
 Val Phe Ser Asp Gln Ser Leu Asn Val Gly Val Phe Gly Gly Ile Gln  
 325 330 335  
 Ile Ala Gly Asn Thr Trp Asp Ser Ser Leu Arg Gly Gln Ile Glu Asn

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340                      345                      350  
 Ser Phe Lys Glu Tyr Pro Thr Pro Thr Asn Phe Gln Phe Leu Phe Asn  
          355                      360                      365  
 Leu Gly Leu Arg Ala His Phe Ala Ser Thr Met His Arg Arg Phe Leu  
          370                      375                      380  
 Ser Ala Ser Gln Ser Ile Gln His Gly Met Glu Phe Gly Val Lys Ile  
 385                      390                      395                      400  
 Pro Ala Ile Asn Gln Arg Tyr Leu Arg Ala Asn Gly Ala Asp Val Asp  
                          405                      410                      415  
 Tyr Arg Arg Leu Tyr Ala Phe Tyr Ile Asn Tyr Thr Ile Gly Phe \*  
                  420                      425                      430

## (2) INFORMATION FOR SEQ ID NO: 83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1197 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS056

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1197

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

ATG GAA TCA GTA AAA ACA GGA AAA ACA AAT AAG GTT GGC AAG AAT ACA                      48  
 Met Glu Ser Val Lys Thr Gly Lys Thr Asn Lys Val Gly Lys Asn Thr  
          435                      440                      445  
 GAG ATG GCT AAT ACA AAG GCA AAT AAA GAG ACT CAT TTT AAA CAA GTG                      96  
 Glu Met Ala Asn Thr Lys Ala Asn Lys Glu Thr His Phe Lys Gln Val  
          450                      455                      460  
 AGC GCC ATT ACA AAT ATA ATC AGA TCA GTT GGT GGG TTT TTT ACA AAA                      144  
 Ser Ala Ile Thr Asn Ile Ile Arg Ser Val Gly Gly Phe Phe Thr Lys  
 465                      470                      475                      480  
 ATT GCA AAG AGA GTT AGA GGA CTT GTA AAA AAA CAC CCC AAG AAA AGC                      192  
 Ile Ala Lys Arg Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser  
                  485                      490                      495  
 AGT GCG GCA TTA GTA GTA TTG ACC CAT ATT GCG TGC AAG AAA GCG AAA                      240  
 Ser Ala Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys Ala Lys  
                  500                      505                      510  
 GAA TTA GAC GAT AAA GTC CAA GAT AAA TCC AAA CAA GCT GAA AAA GAA                      288

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Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu	
515 520 525	
AAT CAA ATC AAT TGG TGG AAA TAT TCA GGA TTA ACA ATA GCG GCA AGT	336
Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Ala Ser	
530 535 540	
TTA TTA TTA GCC GCT TGT AGC GCT GGT GAT ACT GAT AAA CAG ATA GAA	384
Leu Leu Leu Ala Ala Cys Ser Ala Gly Asp Thr Asp Lys Gln Ile Glu	
545 550 555 560	
CTA GAA CAA GAA AAA AAG GAA GCT GAA AAC GCT AGG GAT AGA GCG AAC	432
Leu Glu Gln Glu Lys Lys Glu Ala Glu Asn Ala Arg Asp Arg Ala Asn	
565 570 575	
AAG AGT GGG ATA GAA CTA GAA CAA GAA AGA CAG AAA ACA AAC AAG AGT	480
Lys Ser Gly Ile Glu Leu Glu Gln Glu Arg Gln Lys Thr Asn Lys Ser	
580 585 590	
GGG ATA GAA CTC GCT AAT AGT CAA ATA AAA GCA GAA CAA GAA AGA CAA	528
Gly Ile Glu Leu Ala Asn Ser Gln Ile Lys Ala Glu Gln Glu Arg Gln	
595 600 605	
AAG ACA GAA CAA GAA AAA CAA AAA GCA AAT AAG AGT GCG ATA GAG TTA	576
Lys Thr Glu Gln Glu Lys Gln Lys Ala Asn Lys Ser Ala Ile Glu Leu	
610 615 620	
GAA CAG CAA AAA CAA AAG ACC ATT AAT ACA CAA AGA GAT TTG ATT AAA	624
Glu Gln Gln Lys Gln Lys Thr Ile Asn Thr Gln Arg Asp Leu Ile Lys	
625 630 635 640	
GAA CAG AAA GAT TTC ATT AAA GAA ACA GAA CAA AAT TGC CAA GAA AAT	672
Glu Gln Lys Asp Phe Ile Lys Glu Thr Glu Gln Asn Cys Gln Glu Asn	
645 650 655	
CAT AAT CAA TTC TTT ATT AAA AAA TTA GGA ATT AAG GGT GGC ATT GCT	720
His Asn Gln Phe Phe Ile Lys Lys Leu Gly Ile Lys Gly Gly Ile Ala	
660 665 670	
ATA GAA GTA GAA GCT GAA TGC AAA ACC CCT AAA CCT GCA AAA ACC AAT	768
Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn	
675 680 685	
CAA ACC CCT ATC CAG CCA AAA CAC CTC CCA AAC TCT AAA CAA CCT CAT	816
Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro His	
690 695 700	
TCT CAA AGA GGA TCA AAA GCG CAA GAG TTT ATC GCT TAT TTG CAA AAA	864
Ser Gln Arg Gly Ser Lys Ala Gln Glu Phe Ile Ala Tyr Leu Gln Lys	
705 710 715 720	
GAG CTA GAA TTT CTG CCC TAT TCG CAA AAA GCT ATC GCT AAA CAA GTG	912
Glu Leu Glu Phe Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val	
725 730 735	
AAT TTC TAT AAA CCA AGT TCT ATC GCT TAT TTA GAA CTA GAT CCT AGA	960
Asn Phe Tyr Lys Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro Arg	
740 745 750	

GAT TTT AAG GTT ACA GAA GAA TGG CAA AAA GAA AAT CTA AAA ATA CGC	1008
Asp Phe Lys Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg	
755 760 765	
TCT AAA GCT CAA GCT AAA ATG CTT GAA ATG AGG GAT TTA AAA CCA GAC	1056
Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Asp Leu Lys Pro Asp	
770 775 780	
CCA CAA GCC CAC CTT CCA ACC TCT CAA AGC CTT TTG TTC GTT CAA AAA	1104
Pro Gln Ala His Leu Pro Thr Ser Gln Ser Leu Leu Phe Val Gln Lys	
785 790 795 800	
ATA TTT GCT GAT GTT AAT AAA GAA ATA GAA GCA GTT GCT AAT ACT GAA	1152
Ile Phe Ala Asp Val Asn Lys Glu Ile Glu Ala Val Ala Asn Thr Glu	
805 810 815	
AAG AAA GCA GAA AAA GCG GGT TAT GGT TAT AGT AAA AGG ATG TAG	1197
Lys Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met *	
820 825 830	

## (2) INFORMATION FOR SEQ ID NO: 84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Met Glu Ser Val Lys Thr Gly Lys Thr Asn Lys Val Gly Lys Asn Thr	
1 5 10 15	
Glu Met Ala Asn Thr Lys Ala Asn Lys Glu Thr His Phe Lys Gln Val	
20 25 30	
Ser Ala Ile Thr Asn Ile Ile Arg Ser Val Gly Gly Phe Phe Thr Lys	
35 40 45	
Ile Ala Lys Arg Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser	
50 55 60	
Ser Ala Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys Ala Lys	
65 70 75 80	
Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu	
85 90 95	
Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Ala Ser	
100 105 110	
Leu Leu Leu Ala Ala Cys Ser Ala Gly Asp Thr Asp Lys Gln Ile Glu	
115 120 125	
Leu Glu Gln Glu Lys Lys Glu Ala Glu Asn Ala Arg Asp Arg Ala Asn	
130 135 140	
Lys Ser Gly Ile Glu Leu Glu Gln Glu Arg Gln Lys Thr Asn Lys Ser	

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145                      150                      155                      160  
 Gly Ile Glu Leu Ala Asn Ser Gln Ile Lys Ala Glu Gln Glu Arg Gln  
                                  165                      170                      175  
 Lys Thr Glu Gln Glu Lys Gln Lys Ala Asn Lys Ser Ala Ile Glu Leu  
                                  180                      185                      190  
 Glu Gln Gln Lys Gln Lys Thr Ile Asn Thr Gln Arg Asp Leu Ile Lys  
                                  195                      200                      205  
 Glu Gln Lys Asp Phe Ile Lys Glu Thr Glu Gln Asn Cys Gln Glu Asn  
                                  210                      215                      220  
 His Asn Gln Phe Phe Ile Lys Lys Leu Gly Ile Lys Gly Gly Ile Ala  
 225                                   230                      235                      240  
 Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn  
                                  245                      250                      255  
 Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro His  
                                  260                      265                      270  
 Ser Gln Arg Gly Ser Lys Ala Gln Glu Phe Ile Ala Tyr Leu Gln Lys  
                                  275                      280                      285  
 Glu Leu Glu Phe Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val  
                                  290                      295                      300  
 Asn Phe Tyr Lys Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro Arg  
 305                                   310                      315                      320  
 Asp Phe Lys Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg  
                                  325                      330                      335  
 Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Asp Leu Lys Pro Asp  
                                  340                      345                      350  
 Pro Gln Ala His Leu Pro Thr Ser Gln Ser Leu Leu Phe Val Gln Lys  
                                  355                      360                      365  
 Ile Phe Ala Asp Val Asn Lys Glu Ile Glu Ala Val Ala Asn Thr Glu  
                                  370                      375                      380  
 Lys Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met \*  
 385                                   390                      395

## (2) INFORMATION FOR SEQ ID NO: 85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS059

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## (ix) FEATURES:

(A) NAME/KEY: CDS

(B) POSITION:1..1131

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

ATG AAT TTT TTT AAA ATC CTT TTA ATG GAA TTA AGA GCC ATT GTT TCT	48
Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser	
400 405 410 415	
CAT AAA GGC GTT TTA TTA ATC CTT ATA GGC GCT CCT TTA ATC TAT GGC	96
His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly	
420 425 430	
TTA TTA TAC CCT TTG CCT TAT TTA AGA GAC ATC GTA ACG CAG CAA AAA	144
Leu Leu Tyr Pro Leu Pro Tyr Leu Arg Asp Ile Val Thr Gln Gln Lys	
435 440 445	
ATC GCC CTT GTA GAT GAA GAC AAT TCC TTC CTT TCT AGG CAA TTA GCC	192
Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala	
450 455 460	
TTC ATG GCG CAA AGC TCC AAC GAG TTA GAA ATC GCT TTT TTT AGC CCC	240
Phe Met Ala Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro	
465 470 475	
TCT ATG CTG GAA GCC AAA AAG CTT TTA AAA GAA GAA AAA ATT TAT GGG	288
Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly	
480 485 490 495	
ATC TTG CAC ATT CCC TCT CAT TTT GAA GCC AAT ATC CAT AAA CAA GTG	336
Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile His Lys Gln Val	
500 505 510	
CCT GTA ACG ATA GAT TTT TAT GCG AAT TCC AAT TAC TTT TTG ATT TAT	384
Pro Val Thr Ile Asp Phe Tyr Ala Asn Ser Asn Tyr Phe Leu Ile Tyr	
515 520 525	
GGT GCG TTA GCG AAT GCG GTG GTG GAG AGC ATC AAC GCT TTA AAT GAT	432
Gly Ala Leu Ala Asn Ala Val Val Glu Ser Ile Asn Ala Leu Asn Asp	
530 535 540	
GAG ATA AGG TTC AAA CGC AAT GCC CAA ATA GAA GAA GCT GAA TTA GGG	480
Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu Gly	
545 550 555	
ACA GAC GGG ATT AAA ATC AGG CCT ATC GCT TTA TAT AAC CCT AGT GAG	528
Thr Asp Gly Ile Lys Ile Arg Pro Ile Ala Leu Tyr Asn Pro Ser Glu	
560 565 570 575	
GGG TAT TTG AAT TAC GCG CTC TCT AGC GTG TTT ATT TTC ATT TTG CAC	576
Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile Leu His	
580 585 590	
CAG GTG ATG CTC ATT GCA AGC AGC ATG TTT ACT AGC TCC AGG CGT TTG	624
Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg Arg Leu	
595 600 605	

GAA TTA GCC CTT TTA GAC AGA AAG CAA ATC GCT TTA AGG CTG TGC ACA 672  
 Glu Leu Ala Leu Leu Asp Arg Lys Gln Ile Ala Leu Arg Leu Cys Thr  
 610 615 620

AGA CTT TTG GTG TTC ATG GGG GCG TTT AGC GTT TTT ATT TTA TGG TAT 720  
 Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Ile Leu Trp Tyr  
 625 630 635

TTT GGG GCG CTG TTT TCT TTT TAT GGG ATC GAA CGG CAT GGG AGC GCT 768  
 Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly Ser Ala  
 640 645 650 655

TTA ATG GTG TTT TTG AAT AGT TTG ATT TTC ATG CTT GCA ACC TTG AGT 816  
 Leu Met Val Phe Leu Asn Ser Leu Ile Phe Met Leu Ala Thr Leu Ser  
 660 665 670

TTG GGG TCG TTT TTA GGC GCA TGG ATT AAA AAT GAA GCC CAC ACC ACT 864  
 Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His Thr Thr  
 675 680 685

CAA ATC GTT TTA ATT TCT TCT TTG CCC TTG ATT TTT ATG ATG GGT TTT 912  
 Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met Gly Phe  
 690 695 700

GTG TGG CCT TTT GAA TCC TTG CCC TCT TAT TTA CAG GTT TTT GTT CAA 960  
 Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe Val Gln  
 705 710 715

ATA GTG CCA GCT TAT CAT GGG ATC AGT TTG CTA GGG CGA TTG AAT CAA 1008  
 Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu Asn Gln  
 720 725 730 735

ATG CAT GCG GAA TTT ATA GAT GTT TCC TTC CAT TTT TAT GCG CTT ATT 1056  
 Met His Ala Glu Phe Ile Asp Val Ser Phe His Phe Tyr Ala Leu Ile  
 740 745 750

GCG ATT TTT ATT GCG AGT TTT ATA GGG AGT GTC TTT AAA CTC AGC TCT 1104  
 Ala Ile Phe Ile Ala Ser Phe Ile Gly Ser Val Phe Lys Leu Ser Ser  
 755 760 765

TTA AAG AAA GCT TGT GAA AAC GCT TAA 1131  
 Leu Lys Lys Ala Cys Glu Asn Ala \*  
 770 775

## (2) INFORMATION FOR SEQ ID NO: 86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser  
 1 5 10 15

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His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly  
                   20                                  25                                  30  
 Leu Leu Tyr Pro Leu Pro Tyr Leu Arg Asp Ile Val Thr Gln Gln Lys  
                   35                                  40                                  45  
 Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala  
                   50                                  55                                  60  
 Phe Met Ala Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro  
                   65                                  70                                  75                                  80  
 Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly  
                                   85                                  90                                  95  
 Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile His Lys Gln Val  
                                   100                                  105                                  110  
 Pro Val Thr Ile Asp Phe Tyr Ala Asn Ser Asn Tyr Phe Leu Ile Tyr  
                   115                                  120                                  125  
 Gly Ala Leu Ala Asn Ala Val Val Glu Ser Ile Asn Ala Leu Asn Asp  
                   130                                  135                                  140  
 Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu Gly  
                   145                                  150                                  155                                  160  
 Thr Asp Gly Ile Lys Ile Arg Pro Ile Ala Leu Tyr Asn Pro Ser Glu  
                                   165                                  170                                  175  
 Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile Leu His  
                                   180                                  185                                  190  
 Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg Arg Leu  
                   195                                  200                                  205  
 Glu Leu Ala Leu Leu Asp Arg Lys Gln Ile Ala Leu Arg Leu Cys Thr  
                   210                                  215                                  220  
 Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Ile Leu Trp Tyr  
                   225                                  230                                  235                                  240  
 Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly Ser Ala  
                                   245                                  250                                  255  
 Leu Met Val Phe Leu Asn Ser Leu Ile Phe Met Leu Ala Thr Leu Ser  
                   260                                  265                                  270  
 Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His Thr Thr  
                   275                                  280                                  285  
 Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met Gly Phe  
                   290                                  295                                  300  
 Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe Val Gln  
                   305                                  310                                  315                                  320  
 Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu Asn Gln  
                                   325                                  330                                  335

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Met His Ala Glu Phe Ile Asp Val Ser Phe His Phe Tyr Ala Leu Ile  
 340 345 350

Ala Ile Phe Ile Ala Ser Phe Ile Gly Ser Val Phe Lys Leu Ser Ser  
 355 360 365

Leu Lys Lys Ala Cys Glu Asn Ala \*  
 370 375

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

- (B) CLONE(S): HPS063

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

ATG TTT GTA GTT AAA ATG GTG TTA GGG TTT TTG ATC CTT TTA AGC CCT	48
Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser Pro	
380 385 390	
TTG TGC GCT ACT GGA TTG GAT ATT TCA CAA ACA GAT ATT ATA GAG CGT	96
Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu Arg	
395 400 405	
TCT TTA AAT TTC CTT TTA TTT GTG GGG ATT TTG TGG TAT TTT TCG GCT	144
Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Ser Ala	
410 415 420 425	
AAA AAA CTG CGT TCA TTT TTA CGC TCC AAA AGT CTT GAA ATC TCC AAA	192
Lys Lys Leu Arg Ser Phe Leu Arg Ser Lys Ser Leu Glu Ile Ser Lys	
430 435 440	
CGC TTA GAA GAG ATT CAA GCC CAA CTC AAA GTG AGT AAA GAA AAT AAG	240
Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu Asn Lys	
445 450 455	
AAA AAA CTC TTA AAA GAA TTA GAG CAA GCC AAA GAA AAA GCG GAA TTG	288
Lys Lys Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu Leu	
460 465 470	
ATT GTT TCT GAT GCG AAT AAA GAA GCT TAC ATG ATC ACG CAA AAA TAC	336
Ile Val Ser Asp Ala Asn Lys Glu Ala Tyr Met Ile Thr Gln Lys Tyr	
475 480 485	
GAA TTG CAA ACC AAA ATG GAT GTG GAA AAT TTG ATC AAA AAT TCT AAG	384

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Glu Leu Gln Thr Lys Met Asp Val Glu Asn Leu Ile Lys Asn Ser Lys  
490 495 500 505

GCG TTG ATG GAT TTA GAA GTT AAA AAG ATC AAA AGA GAG CTG GTT GAA 432  
Ala Leu Met Asp Leu Glu Val Lys Lys Ile Lys Arg Glu Leu Val Glu  
510 515 520

AGC GTT TTT AAA GAT CTA AGA GAG AGC AAA AAA GTC TCT TTC AAT GCG 480  
Ser Val Phe Lys Asp Leu Arg Glu Ser Lys Lys Val Ser Phe Asn Ala  
525 530 535

CAA GAT TGC GTG AAT ATT TTG AAA CAA AGG CTT TAA 516  
Gln Asp Cys Val Asn Ile Leu Lys Gln Arg Leu \*  
540 545

## (2) INFORMATION FOR SEQ ID NO: 88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 Amino acids  
(B) TYPE: Amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser Pro  
1 5 10 15

Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu Arg  
20 25 30

Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Ser Ala  
35 40 45

Lys Lys Leu Arg Ser Phe Leu Arg Ser Lys Ser Leu Glu Ile Ser Lys  
50 55 60

Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu Asn Lys  
65 70 75 80

Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu Leu  
85 90 95

Ile Val Ser Asp Ala Asn Lys Glu Ala Tyr Met Ile Thr Gln Lys Tyr  
100 105 110

Glu Leu Gln Thr Lys Met Asp Val Glu Asn Leu Ile Lys Asn Ser Lys  
115 120 125

Ala Leu Met Asp Leu Glu Val Lys Lys Ile Lys Arg Glu Leu Val Glu  
130 135 140

Ser Val Phe Lys Asp Leu Arg Glu Ser Lys Lys Val Ser Phe Asn Ala  
145 150 155 160

Gln Asp Cys Val Asn Ile Leu Lys Gln Arg Leu \*  
165 170

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## (2) INFORMATION FOR SEQ ID NO: 89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS069

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..990

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

ATG TCA AAT AGC ATG TTG GAT AAA AAT AAA GCG ATT CTT ACA GGG GGT	48
Met Ser Asn Ser Met Leu Asp Lys Asn Lys Ala Ile Leu Thr Gly Gly	
175 180 185	
GGG GCT TTA TTG TTA GGG CTA ATC GTG CTT TTT TAT TTG GCT TAT CGC	96
Gly Ala Leu Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg	
190 195 200	
CCT AAG GCT GAA GTG TTG CAA GGA TTT TTG GAA GCC AGA GAA TAC AGC	144
Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser	
205 210 215 220	
GTG AGT TCC AAA GTC CCT GGC CGC ATT GAA AAG GTG TTT GTT AAA AAA	192
Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys	
225 230 235	
GGC GAT CGC ATT AAA AAG GGC GAT TTG GTT TTT AGC ATT TCT AGC CCT	240
Gly Asp Arg Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro	
240 245 250	
GAA TTA GAA GCC AAG CTC GCT CAA GCT GAA GCC GGG CAT AAA GCC GCT	288
Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala	
255 260 265	
AAA GCG CTT AGC GAT GAA GTC AAA AGA GGC TCA AGA GAC GAA ACG ATC	336
Lys Ala Leu Ser Asp Glu Val Lys Arg Gly Ser Arg Asp Glu Thr Ile	
270 275 280	
AAT TCT GCA AGA GAC GTT TGG CAA GCG GCC AAA TCT CAA GCC ACT TTA	384
Asn Ser Ala Arg Asp Val Trp Gln Ala Ala Lys Ser Gln Ala Thr Leu	
285 290 295 300	
GCC AAA GAG ACT TAT AAG CGC GTT CAA GAT TTG TAT GAT AAT GGC GTG	432
Ala Lys Glu Thr Tyr Lys Arg Val Gln Asp Leu Tyr Asp Asn Gly Val	
305 310 315	
GCG AGC TTG CAA AAG CGC GAT GAA GCC TAT GCG GCT TAT GAA AGC ACT	480
Ala Ser Leu Gln Lys Arg Asp Glu Ala Tyr Ala Ala Tyr Glu Ser Thr	
320 325 330	

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AAA TAC AAC GAG AGC GCG GCT TAC CAA AAG TAT AAA ATG GCT TTA GGG 528  
 Lys Tyr Asn Glu Ser Ala Ala Tyr Gln Lys Tyr Lys Met Ala Leu Gly  
 335 340 345

GGG GCG AGC TCT GAA AGT AAG ATT GCC GCT AAG GCT AAA GAG AGC GCG 576  
 Gly Ala Ser Ser Glu Ser Lys Ile Ala Ala Lys Ala Lys Glu Ser Ala  
 350 355 360

GCT TTA GGG CAA GTG AAT GAA GTG GAG TCT TAT TTA AAA GAT GTC AAA 624  
 Ala Leu Gly Gln Val Asn Glu Val Glu Ser Tyr Leu Lys Asp Val Lys  
 365 370 375 380

GCG ACA GCC CCA ATT GAT GGG GAA GTG AGT AAT GTG CTT TTA AGC GGT 672  
 Ala Thr Ala Pro Ile Asp Gly Glu Val Ser Asn Val Leu Leu Ser Gly  
 385 390 395

GGC GAG CTT AGC CCT AAG GGC TTT CCT GTG GTG CTC ATG ATT GAT TTA 720  
 Gly Glu Leu Ser Pro Lys Gly Phe Pro Val Val Leu Met Ile Asp Leu  
 400 405 410

AAG GAT AGT TGG TTA AAA ATC AGC GTG CCT GAA AAG TAT TTG AAC GAT 768  
 Lys Asp Ser Trp Leu Lys Ile Ser Val Pro Glu Lys Tyr Leu Asn Asp  
 415 420 425

TTT AAA GTG GGT AAG GAA TTT GAA GGT TAT ATC CCG GCG TTG AAA AGA 816  
 Phe Lys Val Gly Lys Glu Phe Glu Gly Tyr Ile Pro Ala Leu Lys Arg  
 430 435 440

AGC GCG AAA TTC AGG GTC AAA TAT TTG AGC GTG ATG GGG GAT TTT GCG 864  
 Ser Ala Lys Phe Arg Val Lys Tyr Leu Ser Val Met Gly Asp Phe Ala  
 445 450 455 460

ACT TGG AAA GCG ACG AAT AAT TCC AAC ACT TAC GAC ATG AAA AGC TAT 912  
 Thr Trp Lys Ala Thr Asn Asn Ser Asn Thr Tyr Asp Met Lys Ser Tyr  
 465 470 475

GAA GTG GAG GCC ATA CCC TTA GAA GAG TTG GAA AAT TTT AGG GTA GGG 960  
 Glu Val Glu Ala Ile Pro Leu Glu Glu Leu Glu Asn Phe Arg Val Gly  
 480 485 490

ATG AGC GTG TTA GTT ACC ATT AAA CCT TAA 990  
 Met Ser Val Leu Val Thr Ile Lys Pro \*  
 495 500

## (2) INFORMATION FOR SEQ ID NO: 90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Ser Asn Ser Met Leu Asp Lys Asn Lys Ala Ile Leu Thr Gly Gly  
 1 5 10 15

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Gly Ala Leu Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg  
                   20                                  25                                  30  
 Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser  
                   35                                  40                                  45  
 Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys  
                   50                                  55                                  60  
 Gly Asp Arg Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro  
                   65                                  70                                  75                                  80  
 Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala  
                                   85                                  90                                  95  
 Lys Ala Leu Ser Asp Glu Val Lys Arg Gly Ser Arg Asp Glu Thr Ile  
                                   100                                  105                                  110  
 Asn Ser Ala Arg Asp Val Trp Gln Ala Ala Lys Ser Gln Ala Thr Leu  
                                   115                                  120                                  125  
 Ala Lys Glu Thr Tyr Lys Arg Val Gln Asp Leu Tyr Asp Asn Gly Val  
                                   130                                  135                                  140  
 Ala Ser Leu Gln Lys Arg Asp Glu Ala Tyr Ala Ala Tyr Glu Ser Thr  
                                   145                                  150                                  155                                  160  
 Lys Tyr Asn Glu Ser Ala Ala Tyr Gln Lys Tyr Lys Met Ala Leu Gly  
                                   165                                  170                                  175  
 Gly Ala Ser Ser Glu Ser Lys Ile Ala Ala Lys Ala Lys Glu Ser Ala  
                                   180                                  185                                  190  
 Ala Leu Gly Gln Val Asn Glu Val Glu Ser Tyr Leu Lys Asp Val Lys  
                                   195                                  200                                  205  
 Ala Thr Ala Pro Ile Asp Gly Glu Val Ser Asn Val Leu Leu Ser Gly  
                                   210                                  215                                  220  
 Gly Glu Leu Ser Pro Lys Gly Phe Pro Val Val Leu Met Ile Asp Leu  
                                   225                                  230                                  235                                  240  
 Lys Asp Ser Trp Leu Lys Ile Ser Val Pro Glu Lys Tyr Leu Asn Asp  
                                   245                                  250                                  255  
 Phe Lys Val Gly Lys Glu Phe Glu Gly Tyr Ile Pro Ala Leu Lys Arg  
                                   260                                  265                                  270  
 Ser Ala Lys Phe Arg Val Lys Tyr Leu Ser Val Met Gly Asp Phe Ala  
                                   275                                  280                                  285  
 Thr Trp Lys Ala Thr Asn Asn Ser Asn Thr Tyr Asp Met Lys Ser Tyr  
                                   290                                  295                                  300  
 Glu Val Glu Ala Ile Pro Leu Glu Glu Leu Glu Asn Phe Arg Val Gly  
                                   305                                  310                                  315                                  320  
 Met Ser Val Leu Val Thr Ile Lys Pro \*  
                                   325                                  330

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## (2) INFORMATION FOR SEQ ID NO: 91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS091

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..684

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

ATG GTA TTT GAC AGA ACA ATC AGC GTA AGA GAA AAA AAA GCG GCT AAA	48
Met Val Phe Asp Arg Thr Ile Ser Val Arg Glu Lys Lys Ala Ala Lys	
335 340 345	
ACG CTT GGG ATT ATT GGG ATC GTC TTT TTT ATT TTG TTT GGC ATC GTG	96
Thr Leu Gly Ile Ile Gly Ile Val Phe Phe Ile Leu Phe Gly Ile Val	
350 355 360	
ATA AGC GGG GTG GCT TTT CAA AAA GAG TGG GTG CAA CAA TTG GAT TTA	144
Ile Ser Gly Val Ala Phe Gln Lys Glu Trp Val Gln Gln Leu Asp Leu	
365 370 375	
TTT TTT ATA GAC TTG ATC CGC AAC CCT GCC CCC ATT CAA AAA AGC GCG	192
Phe Phe Ile Asp Leu Ile Arg Asn Pro Ala Pro Ile Gln Lys Ser Ala	
380 385 390	
TGG CTT TCT TTC GTG TTT TTT AGC ACT TGG TTT GCA CAA AGC AAG CTC	240
Trp Leu Ser Phe Val Phe Phe Ser Thr Trp Phe Ala Gln Ser Lys Leu	
395 400 405 410	
ACC ACT CCT ATA GCC TTA CTC ATT GGC TTG TGG TTT GGG TTT CAA AAA	288
Thr Thr Pro Ile Ala Leu Leu Ile Gly Leu Trp Phe Gly Phe Gln Lys	
415 420 425	
CGC ATC GCT TTG GGG GTG TGG TTT TTC TTT AGC ATC TTA TTA GGT GAA	336
Arg Ile Ala Leu Gly Val Trp Phe Phe Phe Ser Ile Leu Leu Gly Glu	
430 435 440	
TTC ACC TTA AAA TCC CTT AAG CTT TTA GTG GCG CGC CCA CGG CCT GTA	384
Phe Thr Leu Lys Ser Leu Lys Leu Leu Val Ala Arg Pro Arg Pro Val	
445 450 455	
ACC AAT GGC GAA TTG GTT TTC GCG CAT GGC TTT AGT TTC CCT AGC GGG	432
Thr Asn Gly Glu Leu Val Phe Ala His Gly Phe Ser Phe Pro Ser Gly	
460 465 470	
CAT GCT TTG GCT TCA GCG CTT TTT TAC GGC TCT TTG GCG TTG TTG TTA	480
His Ala Leu Ala Ser Ala Leu Phe Tyr Gly Ser Leu Ala Leu Leu Leu	

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475	480	485	490	
TGC TAT TCT AAC GCC AAC AAT CGC ATT AAA ACG ATT ATT GCT GTG GTT				528
Cys Tyr Ser Asn Ala Asn Asn Arg Ile Lys Thr Ile Ile Ala Val Val	495	500	505	
TTG CTT TTT TGG ATT TTT TTA ATG GCG TAT GAT AGG GTT TAT TTA GGG				576
Leu Leu Phe Trp Ile Phe Leu Met Ala Tyr Asp Arg Val Tyr Leu Gly	510	515	520	
GTG CAT TAC CCT AGC GAT GTT TTA GGA GGG TTT TTA TTA GGG ATT GCT				624
Val His Tyr Pro Ser Asp Val Leu Gly Gly Phe Leu Leu Gly Ile Ala	525	530	535	
TGG TCG TGC TGC TCT TTA GCG CTT TAT TTA GGG TTT TTG AAA CGC CCT				672
Trp Ser Cys Cys Ser Leu Ala Leu Tyr Leu Gly Phe Leu Lys Arg Pro	540	545	550	
TAT AAT CAA TAA				684
Tyr Asn Gln *				
555				

## (2) INFORMATION FOR SEQ ID NO: 92:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 Amino acids

(B) TYPE: Amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Met Val Phe Asp Arg Thr Ile Ser Val Arg Glu Lys Lys Ala Ala Lys	1	5	10	15
Thr Leu Gly Ile Ile Gly Ile Val Phe Phe Ile Leu Phe Gly Ile Val	20	25	30	
Ile Ser Gly Val Ala Phe Gln Lys Glu Trp Val Gln Gln Leu Asp Leu	35	40	45	
Phe Phe Ile Asp Leu Ile Arg Asn Pro Ala Pro Ile Gln Lys Ser Ala	50	55	60	
Trp Leu Ser Phe Val Phe Phe Ser Thr Trp Phe Ala Gln Ser Lys Leu	65	70	75	80
Thr Thr Pro Ile Ala Leu Leu Ile Gly Leu Trp Phe Gly Phe Gln Lys	85	90	95	
Arg Ile Ala Leu Gly Val Trp Phe Phe Phe Ser Ile Leu Leu Gly Glu	100	105	110	
Phe Thr Leu Lys Ser Leu Lys Leu Leu Val Ala Arg Pro Arg Pro Val	115	120	125	
Thr Asn Gly Glu Leu Val Phe Ala His Gly Phe Ser Phe Pro Ser Gly	130	135	140	

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His Ala Leu Ala Ser Ala Leu Phe Tyr Gly Ser Leu Ala Leu Leu Leu  
145 150 155 160

Cys Tyr Ser Asn Ala Asn Asn Arg Ile Lys Thr Ile Ile Ala Val Val  
165 170 175

Leu Leu Phe Trp Ile Phe Leu Met Ala Tyr Asp Arg Val Tyr Leu Gly  
180 185 190

Val His Tyr Pro Ser Asp Val Leu Gly Gly Phe Leu Leu Gly Ile Ala  
195 200 205

Trp Ser Cys Cys Ser Leu Ala Leu Tyr Leu Gly Phe Leu Lys Arg Pro  
210 215 220

Tyr Asn Gln \*  
225

## (2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 729 Base pairs  
 (B) TYPE: Nucleotide  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

- (vii) DIRECT SOURCE:  
 (B) CLONE(S): HPS095

- (ix) FEATURES:  
 (A) NAME/KEY: CDS  
 (B) POSITION:1..729

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

ATG AAA AAA ATT TTT TCT CAA TCT TTG TTA GCT TTG GTT GTT TCT GTC	48
Met Lys Lys Ile Phe Ser Gln Ser Leu Leu Ala Leu Val Val Ser Val	
230 235 240	
AAT GCG CTA CTA GCT ATG GAT GGT AAT GGC GTG TTT ATA GGG GCG GGT	96
Asn Ala Leu Leu Ala Met Asp Gly Asn Gly Val Phe Ile Gly Ala Gly	
245 250 255 260	
TAT TTG CAA GGA CAA GCC CAA ATG CAT GCG GAT ATT AAT TCT CAA AAA	144
Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp Ile Asn Ser Gln Lys	
265 270 275	
CAA GCC ACT AGC GCT ACT ATC AAG GGG TTT GAT GCG CTT TTA GGG TAT	192
Gln Ala Thr Ser Ala Thr Ile Lys Gly Phe Asp Ala Leu Leu Gly Tyr	
280 285 290	
CAG TTT TTC TTT GGG AAA TAC TTT GGC TTA CGC CTT TAT GGG TTT TTT	240
Gln Phe Phe Phe Gly Lys Tyr Phe Gly Leu Arg Leu Tyr Gly Phe Phe	
295 300 305	

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GAC TAC GCC CAT GCC AAT TCT ATT AGG CTT AAA AAC CCT AAT TAT AAC 288  
 Asp Tyr Ala His Ala Asn Ser Ile Arg Leu Lys Asn Pro Asn Tyr Asn  
 310 315 320

AAC GAA GTG GTG CAA TTG GCG GGT CAA GTT CTT GGG AAA CAA GAA ATC 336  
 Asn Glu Val Val Gln Leu Ala Gly Gln Val Leu Gly Lys Gln Glu Ile  
 325 330 335 340

AAT CGT TTA ACG AGC CTT GCT GAT CCC AAA ACC TTT GAG CCA AAC ATG 384  
 Asn Arg Leu Thr Ser Leu Ala Asp Pro Lys Thr Phe Glu Pro Asn Met  
 345 350 355

CTC ACT TAT GGG GGG GCT ATG GAT GTG ATG GTT AAT GTC ATT AAT AAT 432  
 Leu Thr Tyr Gly Gly Ala Met Asp Val Met Val Asn Val Ile Asn Asn  
 360 365 370

GGC ATC ATG AGT TTG GGG GCT TTT GGT GGG GTG CAA TTA GCC GGC AAT 480  
 Gly Ile Met Ser Leu Gly Ala Phe Gly Gly Val Gln Leu Ala Gly Asn  
 375 380 385

TCA TGG CTT ATG GCG ACG CCG AGC TTT GAG GGC ATT TTA GTG GAG CAA 528  
 Ser Trp Leu Met Ala Thr Pro Ser Phe Glu Gly Ile Leu Val Glu Gln  
 390 395 400

GCT TTG GTG AGC AAG AAA GCC ACT TCT TTC CAA TTT TTA TTC AAT GTG 576  
 Ala Leu Val Ser Lys Lys Ala Thr Ser Phe Gln Phe Leu Phe Asn Val  
 405 410 415 420

GGG GCT CGC TTA AGG ATC TTA AAG CAT TCT AGC ATT GAA GCG GGC GTG 624  
 Gly Ala Arg Leu Arg Ile Leu Lys His Ser Ser Ile Glu Ala Gly Val  
 425 430 435

AAG TTC CCC ATG TTA AAG AAA AAC CCC TAT ATC ACT GCA AAA AAC TTG 672  
 Lys Phe Pro Met Leu Lys Lys Asn Pro Tyr Ile Thr Ala Lys Asn Leu  
 440 445 450

GAT ATA GGG TTT AGG CGC GTG TAT TCA TGG TAT GTG AAT TAT GTG TTC 720  
 Asp Ile Gly Phe Arg Arg Val Tyr Ser Trp Tyr Val Asn Tyr Val Phe  
 455 460 465

ACT TTC TAG 729  
 Thr Phe \*  
 470

## (2) INFORMATION FOR SEQ ID NO: 94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Met Lys Lys Ile Phe Ser Gln Ser Leu Leu Ala Leu Val Val Ser Val  
 1 5 10 15  
 Asn Ala Leu Leu Ala Met Asp Gly Asn Gly Val Phe Ile Gly Ala Gly

00000115 1130001

20 25 30  
 Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp Ile Asn Ser Gln Lys  
 35 40 45  
 Gln Ala Thr Ser Ala Thr Ile Lys Gly Phe Asp Ala Leu Leu Gly Tyr  
 50 55 60  
 Gln Phe Phe Phe Gly Lys Tyr Phe Gly Leu Arg Leu Tyr Gly Phe Phe  
 65 70 75 80  
 Asp Tyr Ala His Ala Asn Ser Ile Arg Leu Lys Asn Pro Asn Tyr Asn  
 85 90 95  
 Asn Glu Val Val Gln Leu Ala Gly Gln Val Leu Gly Lys Gln Glu Ile  
 100 105 110  
 Asn Arg Leu Thr Ser Leu Ala Asp Pro Lys Thr Phe Glu Pro Asn Met  
 115 120 125  
 Leu Thr Tyr Gly Gly Ala Met Asp Val Met Val Asn Val Ile Asn Asn  
 130 135 140  
 Gly Ile Met Ser Leu Gly Ala Phe Gly Gly Val Gln Leu Ala Gly Asn  
 145 150 155 160  
 Ser Trp Leu Met Ala Thr Pro Ser Phe Glu Gly Ile Leu Val Glu Gln  
 165 170 175  
 Ala Leu Val Ser Lys Lys Ala Thr Ser Phe Gln Phe Leu Phe Asn Val  
 180 185 190  
 Gly Ala Arg Leu Arg Ile Leu Lys His Ser Ser Ile Glu Ala Gly Val  
 195 200 205  
 Lys Phe Pro Met Leu Lys Lys Asn Pro Tyr Ile Thr Ala Lys Asn Leu  
 210 215 220  
 Asp Ile Gly Phe Arg Arg Val Tyr Ser Trp Tyr Val Asn Tyr Val Phe  
 225 230 235 240  
 Thr Phe \*

## (2) INFORMATION FOR SEQ ID NO: 95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS099

## (ix) FEATURES:

- (A) NAME/KEY: CDS

09980116-113001

(B) POSITION:1..975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ATG CCG GAA AAT TCT AAA CTA CAA CCT GCT AAG TTA GGG AAA AAT TTT	48
Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe	
245 250 255	
GAC CCT GTG GAT CAT TCT AAC AGG AAT TTT TTC TTT TCT CTC ATT CTG	96
Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu	
260 265 270 275	
TCT GTA TTG TTA CAC TGG TTG ATT TAT TTT TTA TTT GAA CAC AGA GAA	144
Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu	
280 285 290	
GAT TTT TTT CCT TCA AAA CCC AAG CTT GTT AAA TTA AAT CCT GAA AAT	192
Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn	
295 300 305	
TTA TTG GTT TTA AAA AGA GGC CAT TCG CAA GAT CCC AGT AAA AAC ACC	240
Leu Leu Val Leu Lys Arg Gly His Ser Gln Asp Pro Ser Lys Asn Thr	
310 315 320	
CAG GGC GCT CCT AAA CCC ACG CTG GCT GGC CCC CAA AAA CCT CCA ACG	288
Gln Gly Ala Pro Lys Pro Thr Leu Ala Gly Pro Gln Lys Pro Pro Thr	
325 330 335	
CCT CCC ACA CCC CCA ACT CCG CCA ACC CCG CCA ACC CCG CCA AAA CCT	336
Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Lys Pro	
340 345 350 355	
ATA GAA AAG CCT AAG CCT GAG CCT AAA CCA AAA CCC AAA CCT GAA CCC	384
Ile Glu Lys Pro Lys Pro Glu Pro Lys Pro Lys Pro Lys Pro Glu Pro	
360 365 370	
AAA AAG CCC AAT CAT AAA CAC AAG GCT CTT AAA AAA GTG GAA AAA GTG	432
Lys Lys Pro Asn His Lys His Lys Ala Leu Lys Lys Val Glu Lys Val	
375 380 385	
GAA GAG AAA AAA GTA GTA GAG GAG AAA AAA GAA GAG AAA AAA ATC GTA	480
Glu Glu Lys Lys Val Val Glu Glu Lys Lys Glu Glu Lys Lys Ile Val	
390 395 400	
GAG CAG AAA GTA GAA CAA AAA GTA GAG CAG AAA AAA ATA GAA GAG AAA	528
Glu Gln Lys Val Glu Gln Lys Val Glu Gln Lys Lys Ile Glu Glu Lys	
405 410 415	
AAA CCT GTC AAA AAA GAA TTT GAC CCT AAC CAG CTT TCT TTC TTG CCT	576
Lys Pro Val Lys Lys Glu Phe Asp Pro Asn Gln Leu Ser Phe Leu Pro	
420 425 430 435	
AAA GAA GTT GCG CCA CCC AGA CAA GAA AAT AAT AAA GGC TTG GAT AAC	624
Lys Glu Val Ala Pro Pro Arg Gln Glu Asn Asn Lys Gly Leu Asp Asn	
440 445 450	
CAA ACC AGA AGG GAT ATT GAT GAA TTG TAT GGC GAA GAA TTT GGG GAT	672
Gln Thr Arg Arg Asp Ile Asp Glu Leu Tyr Gly Glu Glu Phe Gly Asp	

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455 460 465

TTA GGC ACA GCC GAA AAA GAT TTC ATC AGG AAT AAT TTA AGG GAT ATT 720  
 Leu Gly Thr Ala Glu Lys Asp Phe Ile Arg Asn Asn Leu Arg Asp Ile  
 470 475 480

GGG CGC ATC ACG CAA AAA TAT TTA GAA TAC CCT CAA GTA GCG GCT TAT 768  
 Gly Arg Ile Thr Gln Lys Tyr Leu Glu Tyr Pro Gln Val Ala Ala Tyr  
 485 490 495

TTA GGG CAG GAC GGG ACG AAT GCG GTA GAG TTT TAC TTG CAC CCT AAT 816  
 Leu Gly Gln Asp Gly Thr Asn Ala Val Glu Phe Tyr Leu His Pro Asn  
 500 505 510 515

GGC GAT ATT ACC GAT CTT AAA ATC ATC ATT GGC TCT GAA TAC AAA ATG 864  
 Gly Asp Ile Thr Asp Leu Lys Ile Ile Ile Gly Ser Glu Tyr Lys Met  
 520 525 530

CTT GAT GAC AAC ACC TTA AAG ACC ATT CAG ATC GCT TAT AAG GAT TAC 912  
 Leu Asp Asp Asn Thr Leu Lys Thr Ile Gln Ile Ala Tyr Lys Asp Tyr  
 535 540 545

CCA CGC CCC AAA ACT AAA ACC CTC ATT CGC ATC AGA GTG CGT TAT TAC 960  
 Pro Arg Pro Lys Thr Lys Thr Leu Ile Arg Ile Arg Val Arg Tyr Tyr  
 550 555 560

TTA GGG GGC AAT TAA 975  
 Leu Gly Gly Asn \*  
 565

## (2) INFORMATION FOR SEQ ID NO: 96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe  
 1 5 10 15

Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu  
 20 25 30

Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu  
 35 40 45

Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn  
 50 55 60

Leu Leu Val Leu Lys Arg Gly His Ser Gln Asp Pro Ser Lys Asn Thr  
 65 70 75 80

Gln Gly Ala Pro Lys Pro Thr Leu Ala Gly Pro Gln Lys Pro Pro Thr  
 85 90 95

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Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Lys Pro  
100 105 110

Ile Glu Lys Pro Lys Pro Glu Pro Lys Pro Lys Pro Lys Pro Glu Pro  
115 120 125

Lys Lys Pro Asn His Lys His Lys Ala Leu Lys Lys Val Glu Lys Val  
130 135 140

Glu Glu Lys Lys Val Val Glu Glu Lys Lys Glu Glu Lys Lys Ile Val  
145 150 155 160

Glu Gln Lys Val Glu Gln Lys Val Glu Gln Lys Lys Ile Glu Glu Lys  
165 170 175

Lys Pro Val Lys Lys Glu Phe Asp Pro Asn Gln Leu Ser Phe Leu Pro  
180 185 190

Lys Glu Val Ala Pro Pro Arg Gln Glu Asn Asn Lys Gly Leu Asp Asn  
195 200 205

Gln Thr Arg Arg Asp Ile Asp Glu Leu Tyr Gly Glu Glu Phe Gly Asp  
210 215 220

Leu Gly Thr Ala Glu Lys Asp Phe Ile Arg Asn Asn Leu Arg Asp Ile  
225 230 235 240

Gly Arg Ile Thr Gln Lys Tyr Leu Glu Tyr Pro Gln Val Ala Ala Tyr  
245 250 255

Leu Gly Gln Asp Gly Thr Asn Ala Val Glu Phe Tyr Leu His Pro Asn  
260 265 270

Gly Asp Ile Thr Asp Leu Lys Ile Ile Ile Gly Ser Glu Tyr Lys Met  
275 280 285

Leu Asp Asp Asn Thr Leu Lys Thr Ile Gln Ile Ala Tyr Lys Asp Tyr  
290 295 300

Pro Arg Pro Lys Thr Lys Thr Leu Ile Arg Ile Arg Val Arg Tyr Tyr  
305 310 315 320

Leu Gly Gly Asn \*  
325

## (2) INFORMATION FOR SEQ ID NO: 97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS117 (HPS118, HPS162)

## (ix) FEATURES:

09080115 1130001

(A) NAME/KEY: CDS  
(B) POSITION:1..1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

ATG CCA TAC GCC TTA AGA AAA AGA TTT TTC AAA CGC TTT GCG CTG ATT	48
Met Pro Tyr Ala Leu Arg Lys Arg Phe Phe Lys Arg Phe Ala Leu Ile	
330 335 340	
GTT TCA ACT TTT TGT GCG ATA AGC TTG AAC GCT AAA AGC TAT CTG TTT	96
Val Ser Thr Phe Cys Ala Ile Ser Leu Asn Ala Lys Ser Tyr Leu Phe	
345 350 355	
TCC CCT TTG CCC CCA GCA CAC CAG CAA ATC ATT AAG ACA GAG CCT TGC	144
Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro Cys	
360 365 370	
TCT TTG GAA TGC TTG AAA GAC TTG ATG CTG CAA AAT CAA ATC TTT TCT	192
Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser	
375 380 385	
TTT GTG TCT CAA TAC GAT AAC AAC AAC CAA GAT GAG AGC CTT AAA ACT	240
Phe Val Ser Gln Tyr Asp Asn Asn Asn Gln Asp Glu Ser Leu Lys Thr	
390 395 400 405	
TAT TAT CAT GAC ATA CTC AAT AAA CTC AAC CCC GTA TTC ATC GCT TCT	288
Tyr Tyr His Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala Ser	
410 415 420	
CAA ACT CCA GCT AAA GAA AGC TAT GAG CCT AAG ATT GAA TTA GCG GTT	336
Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala Val	
425 430 435	
TTA CTG CCT AAA AAG GTG GTG GGG CGT TAT GCG ATT TCG GTG ATG AAC	384
Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Ser Val Met Asn	
440 445 450	
ACC CTT TTA GCG TAT TTG AAC ACC AGA AAC AAC GAT TTC AAT ATC CAA	432
Thr Leu Leu Ala Tyr Leu Asn Thr Arg Asn Asn Asp Phe Asn Ile Gln	
455 460 465	
GTC TTT GAC AGC GAT GAA GAA AGC CCT GAA AAA TTA GAG CAA ACC TAT	480
Val Phe Asp Ser Asp Glu Glu Ser Pro Glu Lys Leu Glu Gln Thr Tyr	
470 475 480 485	
AAA GAA ATT GAA AAA GAA AAA TTC CCT TTT GTG ATA GCC TTA TTG ACT	528
Lys Glu Ile Glu Lys Glu Lys Phe Pro Phe Val Ile Ala Leu Leu Thr	
490 495 500	
AAA GAG GGC GTG GAA AAT TTG CTC CAA AAC ACC ACC ATT AGC ACC CCT	576
Lys Glu Gly Val Glu Asn Leu Leu Gln Asn Thr Thr Ile Ser Thr Pro	
505 510 515	
ACT TAT GTG CCT ACG GTG AAT AGA GCG CAA TTG GAA AAT CAA ACT GAA	624
Thr Tyr Val Pro Thr Val Asn Arg Ala Gln Leu Glu Asn Gln Thr Glu	
520 525 530	
CGT TCT TTG AGC GAG CGC TTG TAT TTT GGG GGG ATT GAT TAT AAA GAG	672

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Arg	Ser	Leu	Ser	Glu	Arg	Leu	Tyr	Phe	Gly	Gly	Ile	Asp	Tyr	Lys	Glu	
535						540					545					
CAA	TTA	AGC	ATG	CTC	ACG	GCT	TTC	ATT	AAC	CCT	AAT	TCG	CCC	GTG	ATT	720
Gln	Leu	Ser	Met	Leu	Thr	Ala	Phe	Ile	Asn	Pro	Asn	Ser	Pro	Val	Ile	
550					555					560					565	
GAA	TAC	GAT	GAC	GAT	GGC	CTA	ATA	GGT	GAA	CGC	TTG	AGG	CAA	ATC	ACG	768
Glu	Tyr	Asp	Asp	Asp	Gly	Leu	Ile	Gly	Glu	Arg	Leu	Arg	Gln	Ile	Thr	
				570					575					580		
GAG	TCT	TTA	AGC	ATT	GAA	GTC	AAA	CAC	CAA	GAA	AAT	ATT	TCT	TAC	AAG	816
Glu	Ser	Leu	Ser	Ile	Glu	Val	Lys	His	Gln	Glu	Asn	Ile	Ser	Tyr	Lys	
			585					590					595			
CAA	GCC	ACG	AGT	TTT	TCT	AAA	AAT	TTT	AGA	AAA	AAC	GAT	GCG	TTT	TTT	864
Gln	Ala	Thr	Ser	Phe	Ser	Lys	Asn	Phe	Arg	Lys	Asn	Asp	Ala	Phe	Phe	
	600						605					610				
AAA	AAT	TCT	ATT	TTG	ATT	TTA	AAC	ACC	CCT	ACC	ACT	AAA	AGC	GGC	CTT	912
Lys	Asn	Ser	Ile	Leu	Ile	Leu	Asn	Thr	Pro	Thr	Thr	Lys	Ser	Gly	Leu	
	615					620					625					
ATT	CTT	TCT	CAA	ATA	GGG	CTT	TTA	GAA	TAC	AAG	CCT	CTT	AAA	ATC	CTT	960
Ile	Leu	Ser	Gln	Ile	Gly	Leu	Leu	Glu	Tyr	Lys	Pro	Leu	Lys	Ile	Leu	
630					635					640					645	
TCC	ACA	CAA	ATC	AAT	TTC	AAC	CCC	TCT	CTA	CTC	TTA	CTC	ACC	CAA	CCT	1008
Ser	Thr	Gln	Ile	Asn	Phe	Asn	Pro	Ser	Leu	Leu	Leu	Leu	Thr	Gln	Pro	
				650					655					660		
AAA	GAC	AGA	AAG	GAT	TTA	TTC	ATT	GTC	AAT	GCC	TTG	CAA	AAT	AGC	GAT	1056
Lys	Asp	Arg	Lys	Asp	Leu	Phe	Ile	Val	Asn	Ala	Leu	Gln	Asn	Ser	Asp	
			665					670					675			
GAA	ACG	CTT	ATA	GAA	TAC	GCC	TCC	TTA	TTG	GAG	AGC	GAT	TTA	AGG	CAT	1104
Glu	Thr	Leu	Ile	Glu	Tyr	Ala	Ser	Leu	Leu	Glu	Ser	Asp	Leu	Arg	His	
		680					685					690				
GAT	TGG	GTG	AAT	TAT	TCC	AGC	GCA	ATC	GGG	CTA	GAG	GTG	TTT	TTA	AAC	1152
Asp	Trp	Val	Asn	Tyr	Ser	Ser	Ala	Ile	Gly	Leu	Glu	Val	Phe	Leu	Asn	
	695					700					705					
ACG	CTA	GAT	CCG	CAT	TTT	AAA	AAA	TCT	TTT	CAA	GAG	AAT	TTA	GAA	GAC	1200
Thr	Leu	Asp	Pro	His	Phe	Lys	Lys	Ser	Phe	Gln	Glu	Asn	Leu	Glu	Asp	
710					715					720					725	
AAT	CAG	GTC	CGT	TAC	CAC	AAT	CAA	ATT	TAT	CAG	GCT	TTA	GGG	TAT	TCT	1248
Asn	Gln	Val	Arg	Tyr	His	Asn	Gln	Ile	Tyr	Gln	Ala	Leu	Gly	Tyr	Ser	
				730					735					740		
TTT	GAG	CCA	ATA	AAA	AAT	GAA	AGC	GGA	ACA	AAA	AAA	GAA	TAA			1290
Phe	Glu	Pro	Ile	Lys	Asn	Glu	Ser	Gly	Thr	Lys	Lys	Glu	*			
			745					750					755			

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

09080115-113001



(A) LENGTH: 430 Amino acids  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Met Pro Tyr Ala Leu Arg Lys Arg Phe Phe Lys Arg Phe Ala Leu Ile  
 1 5 10 15  
 Val Ser Thr Phe Cys Ala Ile Ser Leu Asn Ala Lys Ser Tyr Leu Phe  
 20 25 30  
 Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro Cys  
 35 40 45  
 Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser  
 50 55 60  
 Phe Val Ser Gln Tyr Asp Asn Asn Asn Gln Asp Glu Ser Leu Lys Thr  
 65 70 75 80  
 Tyr Tyr His Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala Ser  
 85 90 95  
 Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala Val  
 100 105 110  
 Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Ser Val Met Asn  
 115 120 125  
 Thr Leu Leu Ala Tyr Leu Asn Thr Arg Asn Asn Asp Phe Asn Ile Gln  
 130 135 140  
 Val Phe Asp Ser Asp Glu Glu Ser Pro Glu Lys Leu Glu Gln Thr Tyr  
 145 150 155 160  
 Lys Glu Ile Glu Lys Glu Lys Phe Pro Phe Val Ile Ala Leu Leu Thr  
 165 170 175  
 Lys Glu Gly Val Glu Asn Leu Leu Gln Asn Thr Thr Ile Ser Thr Pro  
 180 185 190  
 Thr Tyr Val Pro Thr Val Asn Arg Ala Gln Leu Glu Asn Gln Thr Glu  
 195 200 205  
 Arg Ser Leu Ser Glu Arg Leu Tyr Phe Gly Gly Ile Asp Tyr Lys Glu  
 210 215 220  
 Gln Leu Ser Met Leu Thr Ala Phe Ile Asn Pro Asn Ser Pro Val Ile  
 225 230 235 240  
 Glu Tyr Asp Asp Asp Gly Leu Ile Gly Glu Arg Leu Arg Gln Ile Thr  
 245 250 255  
 Glu Ser Leu Ser Ile Glu Val Lys His Gln Glu Asn Ile Ser Tyr Lys  
 260 265 270  
 Gln Ala Thr Ser Phe Ser Lys Asn Phe Arg Lys Asn Asp Ala Phe Phe

09930116-113001

(2) INFORMATION FOR SEO ID NO: 99:

(A) LENGTH: 1644 Base pairs  
(B) TYPE: Nucleotide  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(B) CLONE(S) : HPS121

(A) NAME/KEY: CDS  
(B) POSITION:1..1644

ATG	GAT	AAA	AAC	AAC	AAT	AAT	CTC	CGC	TTG	ATT	TTA	GCG	ATC	GCT	CTG	48
Met	Asp	Lys	Asn	Asn	Asn	Asn	Leu	Arg	Leu	Ile	Leu	Ala	Ile	Ala	Leu	
				435					440					445		
TCT	TTC	TTG	TTT	ATC	GCT	CTT	TAT	AGC	TAT	TTT	TTC	CAA	AAA	CCA	AAC	96
Ser	Phe	Leu	Phe	Ile	Ala	Leu	Tyr	Ser	Tyr	Phe	Phe	Gln	Lys	Pro	Asn	
			450					455					460			
AAA	ACA	ACA	ACC	CAA	ACC	ACA	AAG	CAA	GAA	ACA	ACC	AAC	AAC	CAT	ACA	144
Lys	Thr	Thr	Thr	Gln	Thr	Thr	Lys	Gln	Glu	Thr	Thr	Asn	Asn	His	Thr	

465	470	475	
GCA ACA AGT CCT AAC GCG CCC AAC GCC CAA CAT TTT AGC ACC ACT CAA			192
Ala Thr Ser Pro Asn Ala Pro Asn Ala Gln His Phe Ser Thr Thr Gln			
480	485	490	
ACA ACC CCC CAA GAG AAT TTG CTA AGC ACG ATT TCT TTT GAG CAT GCC			240
Thr Thr Pro Gln Glu Asn Leu Leu Ser Thr Ile Ser Phe Glu His Ala			
495	500	505	510
AGG ATT GAA ATT GAT TCT TTA GGG CGC ATC AAA CAG GTT TAT CTC AAG			288
Arg Ile Glu Ile Asp Ser Leu Gly Arg Ile Lys Gln Val Tyr Leu Lys			
515	520	525	
GAT AAA AAG TAT CTA ACC CCT AAA CAA AAG GGC TTT TTA GAG CAT GTG			336
Asp Lys Lys Tyr Leu Thr Pro Lys Gln Lys Gly Phe Leu Glu His Val			
530	535	540	
GGC CAT CTT TTT AGC TCC AAA GAA AAC GCG CAA CCC CCC CTA AAA GAG			384
Gly His Leu Phe Ser Ser Lys Glu Asn Ala Gln Pro Pro Leu Lys Glu			
545	550	555	
CTC CCC CTT TTA GCA GCC GAT AAA CTC AAG CCT TTA GAA GTG CGT TTT			432
Leu Pro Leu Leu Ala Ala Asp Lys Leu Lys Pro Leu Glu Val Arg Phe			
560	565	570	
TTA GAC CCT ACG CTC AAT AAC AAA GCG TTC AAC ACC CCT TAT AGC GCT			480
Leu Asp Pro Thr Leu Asn Asn Lys Ala Phe Asn Thr Pro Tyr Ser Ala			
575	580	585	590
TCA AAA ACC ACT CTT GGG CCT AAC GAA CAG CTT GTT TTA ACC CAA GAT			528
Ser Lys Thr Thr Leu Gly Pro Asn Glu Gln Leu Val Leu Thr Gln Asp			
595	600	605	
TTA GGC ACT CTT AGC ATC ATT AAA ACC CTG ACT TTC TAT GAT GAT TTG			576
Leu Gly Thr Leu Ser Ile Ile Lys Thr Leu Thr Phe Tyr Asp Asp Leu			
610	615	620	
CAT TAT GAT TTA AAA ATC GCA TTC AAA TCG CCC AAT AAC CTT ATC CCT			624
His Tyr Asp Leu Lys Ile Ala Phe Lys Ser Pro Asn Asn Leu Ile Pro			
625	630	635	
AGC TAT GTG ATC ACC AAT GGT TAC AGG CCG GTG GCT GAT TTG GAC AGC			672
Ser Tyr Val Ile Thr Asn Gly Tyr Arg Pro Val Ala Asp Leu Asp Ser			
640	645	650	
TAC ACC TTT TCA GGC GTG CTT TTA GAA AAT AGC GAC AAA AAA ATT GAA			720
Tyr Thr Phe Ser Gly Val Leu Leu Glu Asn Ser Asp Lys Lys Ile Glu			
655	660	665	670
AAA ATT GAA GAT AAA GAC GCT AAA GAA ATC AAA CGC TTT TCT AAC ACC			768
Lys Ile Glu Asp Lys Asp Ala Lys Glu Ile Lys Arg Phe Ser Asn Thr			
675	680	685	
CTC TTT TTA TCC AGC GTG GAT AGG TAT TTC ACC ACC TTG CTT TTC ACT			816
Leu Phe Leu Ser Ser Val Asp Arg Tyr Phe Thr Thr Leu Leu Phe Thr			
690	695	700	
AAA GAT CCT CAA GGT TTT GAA GCC TTA ATT GAT TCA GAA ATC GGC ACT			864

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Lys	Asp	Pro	Gln	Gly	Phe	Glu	Ala	Leu	Ile	Asp	Ser	Glu	Ile	Gly	Thr	
	705						710					715				
AAA	AAC	CCC	TTA	GGG	TTC	ATT	TCC	CTT	AAA	AAT	GAA	GCG	AAT	TTG	CAT	912
Lys	Asn	Pro	Leu	Gly	Phe	Ile	Ser	Leu	Lys	Asn	Glu	Ala	Asn	Leu	His	
	720					725				730						
GGC	TAT	ATT	GGC	CCT	AAG	GAT	TAC	CGC	TCT	TTG	AAA	GCG	ATT	TCA	CCC	960
Gly	Tyr	Ile	Gly	Pro	Lys	Asp	Tyr	Arg	Ser	Leu	Lys	Ala	Ile	Ser	Pro	
	735				740				745						750	
ATG	CTC	ACC	GAT	GTG	ATA	GAG	TAT	GGC	TTA	ATC	ACT	TTC	TTT	GCA	AAA	1008
Met	Leu	Thr	Asp	Val	Ile	Glu	Tyr	Gly	Leu	Ile	Thr	Phe	Phe	Ala	Lys	
				755					760					765		
GGC	GTG	TTT	GTT	TTA	CTG	GAT	TAT	TTG	TAT	CAA	TTC	GTG	GGC	AAT	TGG	1056
Gly	Val	Phe	Val	Leu	Leu	Asp	Tyr	Leu	Tyr	Gln	Phe	Val	Gly	Asn	Trp	
			770					775					780			
GGT	TGG	GCT	ATC	ATT	CTT	TTA	ACG	ATT	ATC	GTG	CGC	ATC	ATC	CTT	TAT	1104
Gly	Trp	Ala	Ile	Ile	Leu	Leu	Thr	Ile	Ile	Val	Arg	Ile	Ile	Leu	Tyr	
		785					790					795				
CCT	TTA	AGC	TAT	AAG	GGC	ATG	GTG	AGC	ATG	CAA	AAG	CTC	AAA	GAA	TTA	1152
Pro	Leu	Ser	Tyr	Lys	Gly	Met	Val	Ser	Met	Gln	Lys	Leu	Lys	Glu	Leu	
	800					805					810					
GCC	CCT	AAA	ATG	AAA	GAA	CTC	CAA	GAA	AAA	TAC	AAG	GGC	GAA	CCC	CAA	1200
Ala	Pro	Lys	Met	Lys	Glu	Leu	Gln	Glu	Lys	Tyr	Lys	Gly	Glu	Pro	Gln	
	815				820				825						830	
AAA	TTG	CAA	GCC	CAC	ATG	ATG	CAG	CTT	TAC	AAA	AAA	CAT	GGG	GCT	AAC	1248
Lys	Leu	Gln	Ala	His	Met	Met	Gln	Leu	Tyr	Lys	Lys	His	Gly	Ala	Asn	
				835					840					845		
CCA	CTA	GGG	GGT	TGT	CTG	CCC	TTA	ATC	TTA	CAA	ATC	CCG	GTG	TTT	TTT	1296
Pro	Leu	Gly	Gly	Cys	Leu	Pro	Leu	Ile	Leu	Gln	Ile	Pro	Val	Phe	Phe	
			850					855					860			
GCC	ATT	TAT	AGA	GTG	CTT	TAT	AAC	GCT	GTG	GAA	TTG	AAA	AGC	TCA	GAG	1344
Ala	Ile	Tyr	Arg	Val	Leu	Tyr	Asn	Ala	Val	Glu	Leu	Lys	Ser	Ser	Glu	
		865					870					875				
TGG	ATC	TTA	TGG	ATT	CAT	GAT	TTA	TCC	ATC	ATG	GAT	CCG	TAT	TTT	ATT	1392
Trp	Ile	Leu	Trp	Ile	His	Asp	Leu	Ser	Ile	Met	Asp	Pro	Tyr	Phe	Ile	
	880					885					890					
TTA	CCG	CTT	CTT	ATG	GGA	GCG	TCT	ATG	TAT	TGG	CAC	CAA	AGC	GTT	ACG	1440
Leu	Pro	Leu	Leu	Met		Gly	Ala	Ser	Met	Tyr	Trp	His	Gln	Ser	Val	
	895				900					905					910	
CCA	AAC	ACC	ATG	ACC	GAT	CCC	ATG	CAA	GCA	AAG	ATT	TTT	AAA	CTC	TTA	1488
Pro	Asn	Thr	Met	Thr	Asp	Pro	Met	Gln	Ala	Lys	Ile	Phe	Lys	Leu	Leu	
				915					920					925		
CCC	CTA	TTA	TTC	ACA	ATC	TTT	TTA	ATC	ACT	TTC	CCG	GCA	GGG	TTA	GTC	1536
Pro	Leu	Leu	Phe	Thr	Ile	Phe	Leu	Ile	Thr	Phe	Pro	Ala	Gly	Leu	Val	
			930					935					940			

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TTG TAT TGG ACC ACG AAC AAC ATC CTT TCG GTG TTG CAA CAA CTC ATC	1584
Leu Tyr Trp Thr Thr Asn Asn Ile Leu Ser Val Leu Gln Gln Leu Ile	
945 950 955	
ATC AAT AAA GTC TTA GAG AAT AAA AAA CGC ATG CAT GCG CAA AAC AAA	1632
Ile Asn Lys Val Leu Glu Asn Lys Lys Arg Met His Ala Gln Asn Lys	
960 965 970	
AAG GAA CAT TGA	1644
Lys Glu His *	
975	

## (2) INFORMATION FOR SEQ ID NO: 100:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 Amino acids

(B) TYPE: Amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Met	Asp	Lys	Asn	Asn	Asn	Asn	Leu	Arg	Leu	Ile	Leu	Ala	Ile	Ala	Leu	
1				5					10					15		
Ser	Phe	Leu	Phe	Ile	Ala	Leu	Tyr	Ser	Tyr	Phe	Phe	Gln	Lys	Pro	Asn	
			20					25					30			
Lys	Thr	Thr	Thr	Gln	Thr	Thr	Lys	Gln	Glu	Thr	Thr	Asn	Asn	His	Thr	
			35				40					45				
Ala	Thr	Ser	Pro	Asn	Ala	Pro	Asn	Ala	Gln	His	Phe	Ser	Thr	Thr	Gln	
			50			55					60					
Thr	Thr	Pro	Gln	Glu	Asn	Leu	Leu	Ser	Thr	Ile	Ser	Phe	Glu	His	Ala	
			65			70				75					80	
Arg	Ile	Glu	Ile	Asp	Ser	Leu	Gly	Arg	Ile	Lys	Gln	Val	Tyr	Leu	Lys	
				85					90					95		
Asp	Lys	Lys	Tyr	Leu	Thr	Pro	Lys	Gln	Lys	Gly	Phe	Leu	Glu	His	Val	
			100					105					110			
Gly	His	Leu	Phe	Ser	Ser	Lys	Glu	Asn	Ala	Gln	Pro	Pro	Leu	Lys	Glu	
			115				120					125				
Leu	Pro	Leu	Leu	Ala	Ala	Asp	Lys	Leu	Lys	Pro	Leu	Glu	Val	Arg	Phe	
			130			135					140					
Leu	Asp	Pro	Thr	Leu	Asn	Asn	Lys	Ala	Phe	Asn	Thr	Pro	Tyr	Ser	Ala	
			145			150				155				160		
Ser	Lys	Thr	Thr	Leu	Gly	Pro	Asn	Glu	Gln	Leu	Val	Leu	Thr	Gln	Asp	
				165				170						175		
Leu	Gly	Thr	Leu	Ser	Ile	Ile	Lys	Thr	Leu	Thr	Phe	Tyr	Asp	Asp	Leu	
				180				185					190			

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His Tyr Asp Leu Lys Ile Ala Phe Lys Ser Pro Asn Asn Leu Ile Pro  
 195 200 205  
 Ser Tyr Val Ile Thr Asn Gly Tyr Arg Pro Val Ala Asp Leu Asp Ser  
 210 215 220  
 Tyr Thr Phe Ser Gly Val Leu Leu Glu Asn Ser Asp Lys Lys Ile Glu  
 225 230 235 240  
 Lys Ile Glu Asp Lys Asp Ala Lys Glu Ile Lys Arg Phe Ser Asn Thr  
 245 250 255  
 Leu Phe Leu Ser Ser Val Asp Arg Tyr Phe Thr Thr Leu Leu Phe Thr  
 260 265 270  
 Lys Asp Pro Gln Gly Phe Glu Ala Leu Ile Asp Ser Glu Ile Gly Thr  
 275 280 285  
 Lys Asn Pro Leu Gly Phe Ile Ser Leu Lys Asn Glu Ala Asn Leu His  
 290 295 300  
 Gly Tyr Ile Gly Pro Lys Asp Tyr Arg Ser Leu Lys Ala Ile Ser Pro  
 305 310 315 320  
 Met Leu Thr Asp Val Ile Glu Tyr Gly Leu Ile Thr Phe Phe Ala Lys  
 325 330 335  
 Gly Val Phe Val Leu Leu Asp Tyr Leu Tyr Gln Phe Val Gly Asn Trp  
 340 345 350  
 Gly Trp Ala Ile Ile Leu Leu Thr Ile Ile Val Arg Ile Ile Leu Tyr  
 355 360 365  
 Pro Leu Ser Tyr Lys Gly Met Val Ser Met Gln Lys Leu Lys Glu Leu  
 370 375 380  
 Ala Pro Lys Met Lys Glu Leu Gln Glu Lys Tyr Lys Gly Glu Pro Gln  
 385 390 395 400  
 Lys Leu Gln Ala His Met Met Gln Leu Tyr Lys Lys His Gly Ala Asn  
 405 410 415  
 Pro Leu Gly Gly Cys Leu Pro Leu Ile Leu Gln Ile Pro Val Phe Phe  
 420 425 430  
 Ala Ile Tyr Arg Val Leu Tyr Asn Ala Val Glu Leu Lys Ser Ser Glu  
 435 440 445  
 Trp Ile Leu Trp Ile His Asp Leu Ser Ile Met Asp Pro Tyr Phe Ile  
 450 455 460  
 Leu Pro Leu Leu Met Gly Ala Ser Met Tyr Trp His Gln Ser Val Thr  
 465 470 475 480  
 Pro Asn Thr Met Thr Asp Pro Met Gln Ala Lys Ile Phe Lys Leu Leu  
 485 490 495  
 Pro Leu Leu Phe Thr Ile Phe Leu Ile Thr Phe Pro Ala Gly Leu Val  
 500 505 510

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Leu Tyr Trp Thr Thr Asn Asn Ile Leu Ser Val Leu Gln Gln Leu Ile  
 515 520 525

Ile Asn Lys Val Leu Glu Asn Lys Lys Arg Met His Ala Gln Asn Lys  
 530 535 540

Lys Glu His \*  
 545

## (2) INFORMATION FOR SEQ ID NO: 101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3063 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS132

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..3063

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

ATG ATG CTC GCT TCC ATT ATT GAA TTT TCC TTA CGC CAA AGA GTG ATC	48
Met Met Leu Ala Ser Ile Ile Glu Phe Ser Leu Arg Gln Arg Val Ile	
550 555 560	
GTG ATT GTT GGT GCG ATT CTT ATT TTA TTT TTT GGG ACT TAT AGT TTT	96
Val Ile Val Gly Ala Ile Leu Ile Leu Phe Phe Gly Thr Tyr Ser Phe	
565 570 575 580	
ATC AAC ACT CCA GTG GAC GCT TTC CCG GAT ATT TCG CCC ACT CAA GTT	144
Ile Asn Thr Pro Val Asp Ala Phe Pro Asp Ile Ser Pro Thr Gln Val	
585 590 595	
AAA ATC ATT TTA AAA CTC CCC GGC TCT AGC CCT GAA GAA ATG GAA AAC	192
Lys Ile Ile Leu Lys Leu Pro Gly Ser Ser Pro Glu Glu Met Glu Asn	
600 605 610	
AAC ATC GTG CGC CCT TTA GAA TTG GAG CTT TTA GGC TTG AAA GGG CAA	240
Asn Ile Val Arg Pro Leu Glu Leu Glu Leu Leu Gly Leu Lys Gly Gln	
615 620 625	
AAA TCT TTA AGG AGT GTT TCA AAA TAT TCT ATT TCA GAT ATT ACG ATA	288
Lys Ser Leu Arg Ser Val Ser Lys Tyr Ser Ile Ser Asp Ile Thr Ile	
630 635 640	
GAT TTT GAT GAC AGC GTG GAT ATT TAT TTA GCG AGG AAT ATT GTC AAT	336
Asp Phe Asp Asp Ser Val Asp Ile Tyr Leu Ala Arg Asn Ile Val Asn	
645 650 655 660	
GAG CGC TTG AGC AGC GTG ATG AAA GAT TTA CCC GTG GGG GTT GAG GGG	384

Glu	Arg	Leu	Ser	Ser	Val	Met	Lys	Asp	Leu	Pro	Val	Gly	Val	Glu	Gly		
				665					670					675			
GGC	ATG	GCG	CCC	ATT	GTT	ACG	CCG	CTA	TCA	GAT	ATC	TTT	ATG	TTC	ACT	432	
Gly	Met	Ala	Pro	Ile	Val	Thr	Pro	Leu	Ser	Asp	Ile	Phe	Met	Phe	Thr		
			680					685				690					
ATT	GAT	GGC	AAT	ATC	ACT	GAG	ATA	GAA	AAA	CGA	CAG	CTT	TTA	GAT	TTT	480	
Ile	Asp	Gly	Asn	Ile	Thr	Glu	Ile	Glu	Lys	Arg	Gln	Leu	Leu	Asp	Phe		
		695					700				705						
GTG	ATC	CGC	CCA	CAA	TTA	AGA	ATG	ATT	AGC	GGC	GTA	GCA	GAT	GTC	AAT	528	
Val	Ile	Arg	Pro	Gln	Leu	Arg	Met	Ile	Ser	Gly	Val	Ala	Asp	Val	Asn		
	710					715				720							
TCC	ATT	GGA	GGC	TTT	AGC	AGA	GCG	TTT	GTG	ATC	GTG	CCG	GAT	TTT	AAT	576	
Ser	Ile	Gly	Gly	Phe	Ser	Arg	Ala	Phe	Val	Ile	Val	Pro	Asp	Phe	Asn		
725					730				735						740		
GAC	ATG	GCA	AGG	CTT	GGG	GTG	AGT	ATT	TCT	GAT	TTA	GAA	TCG	GCT	GTG	624	
Asp	Met	Ala	Arg	Leu	Gly	Val	Ser	Ile	Ser	Asp	Leu	Glu	Ser	Ala	Val		
			745					750						755			
AGA	GTG	AAT	TTA	AGA	AAC	AGC	GGA	GCG	GGG	CGC	GTG	GAT	AGA	GAT	GGC	672	
Arg	Val	Asn	Leu	Arg	Asn	Ser	Gly	Ala	Gly	Arg	Val	Asp	Arg	Asp	Gly		
		760					765						770				
GAA	ACC	TTT	TTA	GTC	AAA	ATC	CAA	ACC	GCT	TCT	TTG	AGT	TTA	GAA	GAC	720	
Glu	Thr	Phe	Leu	Val	Lys	Ile	Gln	Thr	Ala	Ser	Leu	Ser	Leu	Glu	Asp		
	775					780					785						
ATT	GGC	AAA	ATC	ACC	GTT	TCC	ACT	AAT	TTA	GGG	CAT	TTG	CAC	ATT	AAG	768	
Ile	Gly	Lys	Ile	Thr	Val	Ser	Thr	Asn	Leu	Gly	His	Leu	His	Ile	Lys		
	790					795					800						
GAT	TTT	GCG	AAA	GTC	ATC	AGC	CAG	TCT	CGC	ACC	CGT	TTG	GGG	TTT	GTT	816	
Asp	Phe	Ala	Lys	Val	Ile	Ser	Gln	Ser	Arg	Thr	Arg	Leu	Gly	Phe	Val		
805					810				815						820		
ACT	AAA	GAT	GGC	GTG	GGC	GAG	ACC	ACA	GAA	GGC	TTG	GTG	CTT	TCT	TTA	864	
Thr	Lys	Asp	Gly	Val	Gly	Glu	Thr	Thr	Glu	Gly	Leu	Val	Leu	Ser	Leu		
			825						830					835			
AAA	GAC	GCT	AAC	ACC	AAA	GAA	ATC	ATC	ACT	CAA	GTG	TAT	CAA	AAA	CTA	912	
Lys	Asp	Ala	Asn	Thr	Lys	Glu	Ile	Ile	Thr	Gln	Val	Tyr	Gln	Lys	Leu		
		840						845					850				
GAA	GAA	TTA	AAA	CCC	TTT	TTA	CCG	AAT	GGC	GTG	TCC	ATT	AAT	GTT	TTT	960	
Glu	Glu	Leu	Lys	Pro	Phe	Leu	Pro	Asn	Gly	Val	Ser	Ile	Asn	Val	Phe		
	855						860					865					
TAT	GAT	CGC	TCA	GAA	TTT	ACG	CAA	AAA	GCC	ATT	GCC	ACC	GTT	TCT	AAA	1008	
Tyr	Asp	Arg	Ser	Glu	Phe	Thr	Gln	Lys	Ala	Ile	Ala	Thr	Val	Ser	Lys		
	870					875					880						
ACC	CTC	ATT	GAA	GCC	GTT	GTT	TTA	ATC	ATC	ATC	ACG	CTC	TTT	TTA	TTT	1056	
Thr	Leu	Ile	Glu	Ala	Val	Val	Leu	Ile	Ile	Ile	Thr	Leu	Phe	Leu	Phe		
885					890					895					900		



TTA GGG AAT TTG AGG GCG AGC GTG GCT GTG GGG GTG ATT TTA CCT TTA Leu Gly Asn Leu Arg Ala Ser Val Ala Val Gly Val Ile Leu Pro Leu 905 910 915	1104
AGC TTG TCC GTG GCG TTT ATT TTT ATC AAG TTT AGC GAT CTG ACT TTA Ser Leu Ser Val Ala Phe Ile Phe Ile Lys Phe Ser Asp Leu Thr Leu 920 925 930	1152
AAT TTG ATG AGT TTA GGG GGA TTG GTT ATC GCT ATA GGC ATG CTC ATT Asn Leu Met Ser Leu Gly Gly Leu Val Ile Ala Ile Gly Met Leu Ile 935 940 945	1200
GAC TCA GCC GTG GTG GTG GTG GAA AAC GCT TTT GAA AAA TTA AGC GCT Asp Ser Ala Val Val Val Val Glu Asn Ala Phe Glu Lys Leu Ser Ala 950 955 960	1248
AAC ACT AAA ACC ACT AAA CTC CAT GCA ATC TAT CGT TCG TGT AAA GAA Asn Thr Lys Thr Thr Lys Leu His Ala Ile Tyr Arg Ser Cys Lys Glu 965 970 975 980	1296
ATC GCT GTT TCA GTG GTG AGC GGG GTG GTG ATC ATC ATT GTG TTT TTT Ile Ala Val Ser Val Val Ser Gly Val Val Ile Ile Ile Val Phe Phe 985 990 995	1344
GTG CCG ATT TTA ACC TTA CAG GGG TTA GAG GGT AAG ATG TTT AGG CCT Val Pro Ile Leu Thr Leu Gln Gly Leu Glu Gly Lys Met Phe Arg Pro 1000 1005 1010	1392
TTA GCG CAA AGC ATT GTG TAT GCG CTT TTA GGC ACT TTA GTT CTA TCT Leu Ala Gln Ser Ile Val Tyr Ala Leu Leu Gly Thr Leu Val Leu Ser 1015 1020 1025	1440
ATT ACA ATC ATT CCT GTA GTC AGC TCT CTT GTC TTA AAA GCC ACG CCC Ile Thr Ile Ile Pro Val Val Ser Ser Leu Val Leu Lys Ala Thr Pro 1030 1035 1040	1488
CAT AGC GAA ACC TTT TTA ACG AGG TTT TTA AAC AGA ATC TAC GCC CCT His Ser Glu Thr Phe Leu Thr Arg Phe Leu Asn Arg Ile Tyr Ala Pro 1045 1050 1055 1060	1536
TTA TTG GAA TTT TTT GTG CAT AAC CCT AAA AAA GTG ATT TTA GGA GCG Leu Leu Glu Phe Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala 1065 1070 1075	1584
TTT GTT TTT TTA ATC GCA AGC CTT TCT TTA TTC CCT TTT GTG GGG AAG Phe Val Phe Leu Ile Ala Ser Leu Ser Leu Phe Pro Phe Val Gly Lys 1080 1085 1090	1632
AAT TTC ATG CCC GTT TTA GAT GAG GGC GAT GTG GTT TTG AGC GTG GAA Asn Phe Met Pro Val Leu Asp Glu Gly Asp Val Val Leu Ser Val Glu 1095 1100 1105	1680
ACC ACC CCT TCT ATT TCT TTA GAT CAA TCT AGG GAT CTC ATG CTA AAC Thr Thr Pro Ser Ile Ser Leu Asp Gln Ser Arg Asp Leu Met Leu Asn 1110 1115 1120	1728
ATT GAG AGC GCG ATT AAA AAG CAT GTC AAG GAA GTT AAA AGC ATT GTC Ile Glu Ser Ala Ile Lys Lys His Val Lys Glu Val Lys Ser Ile Val 1125 1130 1135 1140	1776

GCG CGC ACA GGG AGC GAT GAA TTG GGG CTG GAT TTA GGA GGT TTG AAT	1824
Ala Arg Thr Gly Ser Asp Glu Leu Gly Leu Asp Leu Gly Gly Leu Asn	
1145 1150 1155	
CAA ACC GAT ACT TTT ATT TCT TTT ATT CCT AAA AAA GAA TGG AGC GTT	1872
Gln Thr Asp Thr Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp Ser Val	
1160 1165 1170	
AAA ACC AAA GAT GAA TTA TTA GAA AAA ATC ATG GAT TCT TTA AAA GAC	1920
Lys Thr Lys Asp Glu Leu Leu Glu Lys Ile Met Asp Ser Leu Lys Asp	
1175 1180 1185	
TTT AAG GGG ATT AAC TTT TCT TTC ACC CAA CCC ATT GAA ATG AGA ATT	1968
Phe Lys Gly Ile Asn Phe Ser Phe Thr Gln Pro Ile Glu Met Arg Ile	
1190 1195 1200	
TCT GAA ATG CTG ACA GGG GTT AGG GGG GAT TTA GCG GTT AAG ATT TTT	2016
Ser Glu Met Leu Thr Gly Val Arg Gly Asp Leu Ala Val Lys Ile Phe	
1205 1210 1215 1220	
GGA GAT GGT ATT AGC GAA TTG AAT GAA TTG AGT TTT CAA ATC GCG CAA	2064
Gly Asp Gly Ile Ser Glu Leu Asn Glu Leu Ser Phe Gln Ile Ala Gln	
1225 1230 1235	
GCT CTA AAA GGG ATT AAA GGA TCT AGT GAA GTT TTA ACC ACG CTT AAT	2112
Ala Leu Lys Gly Ile Lys Gly Ser Ser Glu Val Leu Thr Thr Leu Asn	
1240 1245 1250	
GAG GGC GTG AAT TAT TTG TAT GTA ACC CCT AAT AAA GAA TCG ATG GCG	2160
Glu Gly Val Asn Tyr Leu Tyr Val Thr Pro Asn Lys Glu Ser Met Ala	
1255 1260 1265	
GAT GTG GGG ATC ACT AGC GAT GAA TTT TCC AAG TTT TTA AAA TCC GCT	2208
Asp Val Gly Ile Thr Ser Asp Glu Phe Ser Lys Phe Leu Lys Ser Ala	
1270 1275 1280	
TTA GAG GGC TTG GTT GTA GAT GTG ATC CCT ACA GGG ATT TCA CGC ACG	2256
Leu Glu Gly Leu Val Val Asp Val Ile Pro Thr Gly Ile Ser Arg Thr	
1285 1290 1295 1300	
CCA GTG ATG ATC CGC CAA GAG AGC GAT TTT GCA AGC TCT ATC ACT AAA	2304
Pro Val Met Ile Arg Gln Glu Ser Asp Phe Ala Ser Ser Ile Thr Lys	
1305 1310 1315	
ATC AAA AGT TTA GCC TTG ACT TCA AAA TAT GGC GTT TTA GTG CCT ATC	2352
Ile Lys Ser Leu Ala Leu Thr Ser Lys Tyr Gly Val Leu Val Pro Ile	
1320 1325 1330	
ACT TCT ATC GCC AAA ATT GAA GAA GTG GAT GGC CCT GTT TCT GTT GTG	2400
Thr Ser Ile Ala Lys Ile Glu Glu Val Asp Gly Pro Val Ser Val Val	
1335 1340 1345	
CGT GAA AAT TCA ATG CGC ATG AGC GTG GTT CGC AGT AAT GTG GTG GGG	2448
Arg Glu Asn Ser Met Arg Met Ser Val Val Arg Ser Asn Val Val Gly	
1350 1355 1360	
CGC GAT TTG AAA TCT TTT GTA GAA GAG GCT AAA AAA GTG ATC GCT CAA	2496
Arg Asp Leu Lys Ser Phe Val Glu Glu Ala Lys Lys Val Ile Ala Gln	

1365	1370	1375	1380	
AAC ATC AAA CTC CCT CCC AGC TAC TAT ATC ACT TAT GGG GGG CAG TTT				2544
Asn Ile Lys Leu Pro Pro Ser Tyr Tyr Ile Thr Tyr Gly Gly Gln Phe				
1385	1390	1395		
GAA AAC CAG CAA CGG GCC AAT AAA AGG CTC TCC ACC GTT ATC CCT TTA				2592
Glu Asn Gln Gln Arg Ala Asn Lys Arg Leu Ser Thr Val Ile Pro Leu				
1400	1405	1410		
AGC ATC TTA GCG ATT TTT TTC ATT CTT TTT TTC ACT TTT AAA AGC ATT				2640
Ser Ile Leu Ala Ile Phe Phe Ile Leu Phe Phe Thr Phe Lys Ser Ile				
1415	1420	1425		
CCT TTA GCC TTG CTC ATT CTT TTG AAT ATC CCT TTT GCG GTT ACC GGA				2688
Pro Leu Ala Leu Leu Ile Leu Leu Asn Ile Pro Phe Ala Val Thr Gly				
1430	1435	1440		
GGC CTT ATT GCG TTG TTT GCG GTC GGG GAG TAT ATT TCA GTG CCA GCG				2736
Gly Leu Ile Ala Leu Phe Ala Val Gly Glu Tyr Ile Ser Val Pro Ala				
1445	1450	1455	1460	
AGC GTG GGC TTT ATC GCT CTT TTT GGG ATT GCG GTT TTA AAT GGC GTG				2784
Ser Val Gly Phe Ile Ala Leu Phe Gly Ile Ala Val Leu Asn Gly Val				
1465	1470	1475		
GTG ATG ATA GGC TAT TTT AAA GAG CTT CTC TTG CAA GGG AAA AGC GTA				2832
Val Met Ile Gly Tyr Phe Lys Glu Leu Leu Leu Gln Gly Lys Ser Val				
1480	1485	1490		
GAA GAA TGC GTT TTA TTG GGC GCT AAA AGG CGT TTG AGA CCG GTT TTA				2880
Glu Glu Cys Val Leu Leu Gly Ala Lys Arg Arg Leu Arg Pro Val Leu				
1495	1500	1505		
ATG ACC GCT TGC ATT GCC GGT TTG GGT TTG CTC CCT TTA TTA TTT TCT				2928
Met Thr Ala Cys Ile Ala Gly Leu Gly Leu Leu Pro Leu Leu Phe Ser				
1510	1515	1520		
CAT AGC GTG GGA TCA GAA GTC CAA AAA CCT TTA GCG ATC GTG GTG CTT				2976
His Ser Val Gly Ser Glu Val Gln Lys Pro Leu Ala Ile Val Val Leu				
1525	1530	1535	1540	
GGA GGC TTG GTT ACC TCA AGC GCT CTA ACC TTA CTC CTA CTG CCG CCA				3024
Gly Gly Leu Val Thr Ser Ser Ala Leu Thr Leu Leu Leu Leu Pro Pro				
1545	1550	1555		
ATG TTT ATG CTC ATC GCT AAA AAG ATT AAA ATC GTT TGA				3063
Met Phe Met Leu Ile Ala Lys Lys Ile Lys Ile Val *				
1560	1565			

## (2) INFORMATION FOR SEQ ID NO: 102:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1021 Amino acids

(B) TYPE: Amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Met	Met	Leu	Ala	Ser	Ile	Ile	Glu	Phe	Ser	Leu	Arg	Gln	Arg	Val	Ile	1	5	10	15
Val	Ile	Val	Gly	Ala	Ile	Leu	Ile	Leu	Phe	Phe	Gly	Thr	Tyr	Ser	Phe	20	25	30	
Ile	Asn	Thr	Pro	Val	Asp	Ala	Phe	Pro	Asp	Ile	Ser	Pro	Thr	Gln	Val	35	40	45	
Lys	Ile	Ile	Leu	Lys	Leu	Pro	Gly	Ser	Ser	Pro	Glu	Glu	Met	Glu	Asn	50	55	60	
Asn	Ile	Val	Arg	Pro	Leu	Glu	Leu	Glu	Leu	Leu	Gly	Leu	Lys	Gly	Gln	65	70	75	
Lys	Ser	Leu	Arg	Ser	Val	Ser	Lys	Tyr	Ser	Ile	Ser	Asp	Ile	Thr	Ile	85	90	95	
Asp	Phe	Asp	Asp	Ser	Val	Asp	Ile	Tyr	Leu	Ala	Arg	Asn	Ile	Val	Asn	100	105	110	
Glu	Arg	Leu	Ser	Ser	Val	Met	Lys	Asp	Leu	Pro	Val	Gly	Val	Glu	Gly	115	120	125	
Gly	Met	Ala	Pro	Ile	Val	Thr	Pro	Leu	Ser	Asp	Ile	Phe	Met	Phe	Thr	130	135	140	
Ile	Asp	Gly	Asn	Ile	Thr	Glu	Ile	Glu	Lys	Arg	Gln	Leu	Leu	Asp	Phe	145	150	155	
Val	Ile	Arg	Pro	Gln	Leu	Arg	Met	Ile	Ser	Gly	Val	Ala	Asp	Val	Asn	165	170	175	
Ser	Ile	Gly	Gly	Phe	Ser	Arg	Ala	Phe	Val	Ile	Val	Pro	Asp	Phe	Asn	180	185	190	
Asp	Met	Ala	Arg	Leu	Gly	Val	Ser	Ile	Ser	Asp	Leu	Glu	Ser	Ala	Val	195	200	205	
Arg	Val	Asn	Leu	Arg	Asn	Ser	Gly	Ala	Gly	Arg	Val	Asp	Arg	Asp	Gly	210	215	220	
Glu	Thr	Phe	Leu	Val	Lys	Ile	Gln	Thr	Ala	Ser	Leu	Ser	Leu	Glu	Asp	225	230	235	
Ile	Gly	Lys	Ile	Thr	Val	Ser	Thr	Asn	Leu	Gly	His	Leu	His	Ile	Lys	245	250	255	
Asp	Phe	Ala	Lys	Val	Ile	Ser	Gln	Ser	Arg	Thr	Arg	Leu	Gly	Phe	Val	260	265	270	
Thr	Lys	Asp	Gly	Val	Gly	Glu	Thr	Thr	Glu	Gly	Leu	Val	Leu	Ser	Leu	275	280	285	
Lys	Asp	Ala	Asn	Thr	Lys	Glu	Ile	Ile	Thr	Gln	Val	Tyr	Gln	Lys	Leu	290	295	300	

Glu Glu Leu Lys Pro Phe Leu Pro Asn Gly Val Ser Ile Asn Val Phe  
 305 310 315 320  
 Tyr Asp Arg Ser Glu Phe Thr Gln Lys Ala Ile Ala Thr Val Ser Lys  
 325 330 335  
 Thr Leu Ile Glu Ala Val Val Leu Ile Ile Ile Thr Leu Phe Leu Phe  
 340 345 350  
 Leu Gly Asn Leu Arg Ala Ser Val Ala Val Gly Val Ile Leu Pro Leu  
 355 360 365  
 Ser Leu Ser Val Ala Phe Ile Phe Ile Lys Phe Ser Asp Leu Thr Leu  
 370 375 380  
 Asn Leu Met Ser Leu Gly Gly Leu Val Ile Ala Ile Gly Met Leu Ile  
 385 390 395 400  
 Asp Ser Ala Val Val Val Val Glu Asn Ala Phe Glu Lys Leu Ser Ala  
 405 410 415  
 Asn Thr Lys Thr Thr Lys Leu His Ala Ile Tyr Arg Ser Cys Lys Glu  
 420 425 430  
 Ile Ala Val Ser Val Val Ser Gly Val Val Ile Ile Ile Val Phe Phe  
 435 440 445  
 Val Pro Ile Leu Thr Leu Gln Gly Leu Glu Gly Lys Met Phe Arg Pro  
 450 455 460  
 Leu Ala Gln Ser Ile Val Tyr Ala Leu Leu Gly Thr Leu Val Leu Ser  
 465 470 475 480  
 Ile Thr Ile Ile Pro Val Val Ser Ser Leu Val Leu Lys Ala Thr Pro  
 485 490 495  
 His Ser Glu Thr Phe Leu Thr Arg Phe Leu Asn Arg Ile Tyr Ala Pro  
 500 505 510  
 Leu Leu Glu Phe Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala  
 515 520 525  
 Phe Val Phe Leu Ile Ala Ser Leu Ser Leu Phe Pro Phe Val Gly Lys  
 530 535 540  
 Asn Phe Met Pro Val Leu Asp Glu Gly Asp Val Val Leu Ser Val Glu  
 545 550 555 560  
 Thr Thr Pro Ser Ile Ser Leu Asp Gln Ser Arg Asp Leu Met Leu Asn  
 565 570 575  
 Ile Glu Ser Ala Ile Lys Lys His Val Lys Glu Val Lys Ser Ile Val  
 580 585 590  
 Ala Arg Thr Gly Ser Asp Glu Leu Gly Leu Asp Leu Gly Gly Leu Asn  
 595 600 605  
 Gln Thr Asp Thr Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp Ser Val  
 610 615 620

Lys Thr Lys Asp Glu Leu Leu Glu Lys Ile Met Asp Ser Leu Lys Asp  
 625 630 635 640  
 Phe Lys Gly Ile Asn Phe Ser Phe Thr Gln Pro Ile Glu Met Arg Ile  
 645 650 655  
 Ser Glu Met Leu Thr Gly Val Arg Gly Asp Leu Ala Val Lys Ile Phe  
 660 665 670  
 Gly Asp Gly Ile Ser Glu Leu Asn Glu Leu Ser Phe Gln Ile Ala Gln  
 675 680 685  
 Ala Leu Lys Gly Ile Lys Gly Ser Ser Glu Val Leu Thr Thr Leu Asn  
 690 695 700  
 Glu Gly Val Asn Tyr Leu Tyr Val Thr Pro Asn Lys Glu Ser Met Ala  
 705 710 715 720  
 Asp Val Gly Ile Thr Ser Asp Glu Phe Ser Lys Phe Leu Lys Ser Ala  
 725 730 735  
 Leu Glu Gly Leu Val Val Asp Val Ile Pro Thr Gly Ile Ser Arg Thr  
 740 745 750  
 Pro Val Met Ile Arg Gln Glu Ser Asp Phe Ala Ser Ser Ile Thr Lys  
 755 760 765  
 Ile Lys Ser Leu Ala Leu Thr Ser Lys Tyr Gly Val Leu Val Pro Ile  
 770 775 780  
 Thr Ser Ile Ala Lys Ile Glu Glu Val Asp Gly Pro Val Ser Val Val  
 785 790 795 800  
 Arg Glu Asn Ser Met Arg Met Ser Val Val Arg Ser Asn Val Val Gly  
 805 810 815  
 Arg Asp Leu Lys Ser Phe Val Glu Glu Ala Lys Lys Val Ile Ala Gln  
 820 825 830  
 Asn Ile Lys Leu Pro Pro Ser Tyr Tyr Ile Thr Tyr Gly Gly Gln Phe  
 835 840 845  
 Glu Asn Gln Gln Arg Ala Asn Lys Arg Leu Ser Thr Val Ile Pro Leu  
 850 855 860  
 Ser Ile Leu Ala Ile Phe Phe Ile Leu Phe Phe Thr Phe Lys Ser Ile  
 865 870 875 880  
 Pro Leu Ala Leu Leu Ile Leu Leu Asn Ile Pro Phe Ala Val Thr Gly  
 885 890 895  
 Gly Leu Ile Ala Leu Phe Ala Val Gly Glu Tyr Ile Ser Val Pro Ala  
 900 905 910  
 Ser Val Gly Phe Ile Ala Leu Phe Gly Ile Ala Val Leu Asn Gly Val  
 915 920 925  
 Val Met Ile Gly Tyr Phe Lys Glu Leu Leu Leu Gln Gly Lys Ser Val

930		935		940
Glu Glu Cys Val Leu Leu Gly Ala Lys Arg Arg Leu Arg Pro Val Leu				
945		950		955 960
Met Thr Ala Cys Ile Ala Gly Leu Gly Leu Leu Pro Leu Leu Phe Ser				
	965		970	975
His Ser Val Gly Ser Glu Val Gln Lys Pro Leu Ala Ile Val Val Leu				
	980		985	990
Gly Gly Leu Val Thr Ser Ser Ala Leu Thr Leu Leu Leu Leu Pro Pro				
	995		1000	1005
Met Phe Met Leu Ile Ala Lys Lys Ile Lys Ile Val *				
1010		1015		1020

## (2) INFORMATION FOR SEQ ID NO: 103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2028 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS149

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..2028

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTG TCT AAA GGT TTG AGT ATC GGT AAT AAA ATC ATA TTG TGC GTG GCG	48
Leu Ser Lys Gly Leu Ser Ile Gly Asn Lys Ile Ile Leu Cys Val Ala	
1025 1030 1035	
TTG ATT GTG ATC GTG TGC GTG AGC ATT TTA GGG GTG TCC TTA AAC AGC	96
Leu Ile Val Ile Val Cys Val Ser Ile Leu Gly Val Ser Leu Asn Ser	
1040 1045 1050	
AGG GTG AAA GAG ATT TTA AAA GAA AGC GCT CTG CAT TCT ATG CAA GAT	144
Arg Val Lys Glu Ile Leu Lys Glu Ser Ala Leu His Ser Met Gln Asp	
1055 1060 1065	
AGT TTG CAT TTT AAG GTT AAT GAA GTG CAA GGG GTT TTA GAA AAC ACT	192
Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu Glu Asn Thr	
1070 1075 1080 1085	
TAT ACG AGC ATG GGC ATT GTT AAA GAA ATG CTC CCT AAA GAC ACC AAA	240
Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys Asp Thr Lys	
1090 1095 1100	
AGA GAA ATC AAA ATC GGC TTG TTA AAA AAC TTC ATT TTA GCC AAT TCG	288
Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu Ala Asn Ser	

1105	1110	1115	
CAT GTC GCT GGG GTG AGC ATG TTT TTT AAA GGC AGA GAA GAT TTA AGA His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu Asp Leu Arg 1120 1125 1130			336
TTA ACG CTT TTA AGG GAT AAC AAT ACG ATT AAG CTA GTG GAA AAT CCG Leu Thr Leu Leu Arg Asp Asn Asn Thr Ile Lys Leu Val Glu Asn Pro 1135 1140 1145			384
TCA TTA GAG AAT AGC CCT TTA GCG CAA AAA GCG ATG AAA AAT AAA GAA Ser Leu Glu Asn Ser Pro Leu Ala Gln Lys Ala Met Lys Asn Lys Glu 1150 1155 1160 1165			432
ATT TCT AAA AGT TTG GGT TAT TAT AGG AAA ATG CCT AAT GGG GCG GAA Ile Ser Lys Ser Leu Gly Tyr Tyr Arg Lys Met Pro Asn Gly Ala Glu 1170 1175 1180			480
GTT TAT GGG GTG GAT ATT CTT TTA CCT TTA TTG AAT GAG AAC GCT CAA Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu Asn Ala Gln 1185 1190 1195			528
GAG GTT GTA GGG GCT TTG ATG ATT TTT ATT TCC ATT GAC AGC TTC AGC Glu Val Val Gly Ala Leu Met Ile Phe Ile Ser Ile Asp Ser Phe Ser 1200 1205 1210			576
AAT GAA ATC ACT AAA AAC AGG AGC GAT TTA TTT TTA ATT GGC ACT AAA Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu Phe Leu Ile Gly Thr Lys 1215 1220 1225			624
GGT AAA GTG CTT TTG AGC GCG AAT AAG AGT TTG CAA GAC AAA CCT ATC Gly Lys Val Leu Leu Ser Ala Asn Lys Ser Leu Gln Asp Lys Pro Ile 1230 1235 1240 1245			672
GCA GAA ATT TAT AAG AGC GTG CCT AAA GCC ACC AAC GAA GTG ATG GCT Ala Glu Ile Tyr Lys Ser Val Pro Lys Ala Thr Asn Glu Val Met Ala 1250 1255 1260			720
ATT TTA GAA AAC GGC TCT AAA GCG ACT TTA GAA TAC TTA GAT CCC TTT Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu Glu Tyr Leu Asp Pro Phe 1265 1270 1275			768
AGC CAT AAG GAA AAT TTT TTA GCC GTT GAA ACC TTT AAA ATG CTA GGC Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe Lys Met Leu Gly 1280 1285 1290			816
AAA ACA GAA AGT AAA GAC AAT CTT AAT TGG ATG ATC GCT TTA ATC ATT Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile Ala Leu Ile Ile 1295 1300 1305			864
GAA AAA GAC AAG GTC TAT GAG CAA GTA GGC TCG GTG CGT TTT GTG GTG Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val Arg Phe Val Val 1310 1315 1320 1325			912
ATC ATA GCG AGC GCA ATC ATG GTG TTA GCC TTG ATT ATA GCG ATC ACT Ile Ile Ala Ser Ala Ile Met Val Leu Ala Leu Ile Ile Ala Ile Thr 1330 1335 1340			960
CTC TTA ATG CGA GCG ATC GTG AGC AGT CGT TTG GAA GCC GTT TCT AGC			1008



Leu	Leu	Met	Arg	Ala	Ile	Val	Ser	Ser	Arg	Leu	Glu	Ala	Val	Ser	Ser	
			1345					1350						1355		
ACC	TTG	TCT	CAT	TTC	TTT	AAA	TTA	TTG	AAC	AAT	CAA	GCC	AAT	TCT	AGC	1056
Thr	Leu	Ser	His	Phe	Phe	Lys	Leu	Leu	Asn	Asn	Gln	Ala	Asn	Ser	Ser	
			1360					1365					1370			
GGT	ATT	AAA	TTG	ATT	GAA	GCG	AAA	TCC	AAT	GAC	GAG	TTA	GGC	CGC	ATG	1104
Gly	Ile	Lys	Leu	Ile	Glu	Ala	Lys	Ser	Asn	Asp	Glu	Leu	Gly	Arg	Met	
			1375				1380					1385				
CAA	ACA	GCG	ATC	AAT	AAA	AAT	ATC	TTG	CAA	ACC	CAA	AAA	ATC	ATG	CAA	1152
Gln	Thr	Ala	Ile	Asn	Lys	Asn	Ile	Leu	Gln	Thr	Gln	Lys	Ile	Met	Gln	
			1390				1395				1400				1405	
GAA	GAC	AGG	CAA	GCC	GTC	CAA	GAC	ACC	ATT	AAA	GTG	GTT	TCA	GAT	GTG	1200
Glu	Asp	Arg	Gln	Ala	Val	Gln	Asp	Thr	Ile	Lys	Val	Val	Ser	Asp	Val	
				1410					1415					1420		
AAA	GCA	GGG	AAT	TTT	GCG	GTG	CGC	ATC	ACG	GCT	GAG	CCC	GCA	AGC	CCT	1248
Lys	Ala	Gly	Asn	Phe	Ala	Val	Arg	Ile	Thr	Ala	Glu	Pro	Ala	Ser	Pro	
			1425					1430					1435			
GAT	TTG	AAA	GAA	TTG	AGG	GAC	GCG	CTA	AAT	GGG	ATC	ATG	GAT	TAT	TTG	1296
Asp	Leu	Lys	Glu	Leu	Arg	Asp	Ala	Leu	Asn	Gly	Ile	Met	Asp	Tyr	Leu	
			1440				1445					1450				
CAA	GAA	AGC	GTA	GGG	ACT	CAC	ATG	CCA	AGC	ATT	TTC	AAA	ATC	TTT	GAA	1344
Gln	Glu	Ser	Val	Gly	Thr	His	Met	Pro	Ser	Ile	Phe	Lys	Ile	Phe	Glu	
			1455				1460					1465				
AGC	TAT	TCT	GGT	TTG	GAT	TTT	AGA	GGC	CGG	ATC	CAA	AAC	GCT	TCG	GGT	1392
Ser	Tyr	Ser	Gly	Leu	Asp	Phe	Arg	Gly	Arg	Ile	Gln	Asn	Ala	Ser	Gly	
	1470				1475				1480					1485		
AGG	GTG	GAA	CTG	GTT	ACT	AAC	GCT	TTA	GGG	CAA	GAA	ATC	CAA	AAA	ATG	1440
Arg	Val	Glu	Leu	Val	Thr	Asn	Ala	Leu	Gly	Gln	Glu	Ile	Gln	Lys	Met	
				1490					1495					1500		
CTA	GAA	ACT	TCG	TCT	AAT	TTT	GCC	AAA	GAT	TTA	GCG	AAC	GAT	AGC	GCG	1488
Leu	Glu	Thr	Ser	Ser	Asn	Phe	Ala	Lys	Asp	Leu	Ala	Asn	Asp	Ser	Ala	
			1505					1510					1515			
AAT	TTA	AAA	GAG	TGC	GTG	CAA	AAT	TTA	GAA	AAA	GCT	TCA	AAC	TCC	CAA	1536
Asn	Leu	Lys	Glu	Cys	Val	Gln	Asn	Leu	Glu	Lys	Ala	Ser	Asn	Ser	Gln	
			1520				1525					1530				
CAC	AAA	AGC	TTG	ATG	GAA	ACT	TCC	AAA	ACG	ATA	GAA	AAT	ATC	ACC	ACT	1584
His	Lys	Ser	Leu	Met	Glu	Thr	Ser	Lys	Thr	Ile	Glu	Asn	Ile	Thr	Thr	
			1535				1540				1545					
TCC	ATT	CAA	GGC	GTG	AGC	TCT	CAA	AGT	GAA	GCC	ATG	ATT	GAA	CAA	GGG	1632
Ser	Ile	Gln	Gly	Val	Ser	Ser	Gln	Ser	Glu	Ala	Met	Ile	Glu	Gln	Gly	
	1550				1555					1560				1565		
CAA	GAC	ATT	AAA	AGC	ATT	GTA	GAA	ATC	ATT	AGA	GAT	ATT	GCT	GAT	CAA	1680
Gln	Asp	Ile	Lys	Ser	Ile	Val	Glu	Ile	Ile	Arg	Asp	Ile	Ala	Asp	Gln	
				1570				1575					1580			

ACC AAT CTT TTA GCC TTA AAC GCC GCT ATT GAA GCC GCA AGG GCC GGC Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly 1585 1590 1595	1728
GAG CAT GGC AGA GGC TTT GCG GTG GTG GCT GAT GAG GTA AGA AAG CTC Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg Lys Leu 1600 1605 1610	1776
GCT GAA AGG ACG CAA AAA TCG CTC AGC GAG ATT GAA GCC AAT ATC AAT Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile Glu Ala Asn Ile Asn 1615 1620 1625	1824
ATT TTA GTG CAA AGC ATT TCA GAC ACG AGC GAA AGC ATT AAA AAC CAG Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu Ser Ile Lys Asn Gln 1630 1635 1640 1645	1872
GTT AAA GAA GTG GAA GAA ATC AAC GCT TCT ATT GAA GCC TTA AGA TCG Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu Arg Ser 1650 1655 1660	1920
GTT ACT GAG GGC AAT CTA AAA ATC GCT AGC GAT TCT TTA GAA ATC AGT Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu Ile Ser 1665 1670 1675	1968
CAA GAA ATT GAC AAA GTT TCT AAC GAT ATT TTA GAA GAT GTG AAT AAA Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val Asn Lys 1680 1685 1690	2016
AAG CAG TTT TAA Lys Gln Phe * 1695	2028

## (2) INFORMATION FOR SEQ ID NO: 104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Leu Ser Lys Gly Leu Ser Ile Gly Asn Lys Ile Ile Leu Cys Val Ala 1 5 10 15
Leu Ile Val Ile Val Cys Val Ser Ile Leu Gly Val Ser Leu Asn Ser 20 25 30
Arg Val Lys Glu Ile Leu Lys Glu Ser Ala Leu His Ser Met Gln Asp 35 40 45
Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu Glu Asn Thr 50 55 60
Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys Asp Thr Lys 65 70 75 80
Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu Ala Asn Ser

	85		90		95
His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu Asp Leu Arg	100		105		110
Leu Thr Leu Leu Arg Asp Asn Asn Thr Ile Lys Leu Val Glu Asn Pro	115		120		125
Ser Leu Glu Asn Ser Pro Leu Ala Gln Lys Ala Met Lys Asn Lys Glu	130		135		140
Ile Ser Lys Ser Leu Gly Tyr Tyr Arg Lys Met Pro Asn Gly Ala Glu	145		150		155
Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu Asn Ala Gln	165		170		175
Glu Val Val Gly Ala Leu Met Ile Phe Ile Ser Ile Asp Ser Phe Ser	180		185		190
Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu Phe Leu Ile Gly Thr Lys	195		200		205
Gly Lys Val Leu Leu Ser Ala Asn Lys Ser Leu Gln Asp Lys Pro Ile	210		215		220
Ala Glu Ile Tyr Lys Ser Val Pro Lys Ala Thr Asn Glu Val Met Ala	225		230		235
Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu Glu Tyr Leu Asp Pro Phe	245		250		255
Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe Lys Met Leu Gly	260		265		270
Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile Ala Leu Ile Ile	275		280		285
Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val Arg Phe Val Val	290		295		300
Ile Ile Ala Ser Ala Ile Met Val Leu Ala Leu Ile Ile Ala Ile Thr	305		310		315
Leu Leu Met Arg Ala Ile Val Ser Ser Arg Leu Glu Ala Val Ser Ser	325		330		335
Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln Ala Asn Ser Ser	340		345		350
Gly Ile Lys Leu Ile Glu Ala Lys Ser Asn Asp Glu Leu Gly Arg Met	355		360		365
Gln Thr Ala Ile Asn Lys Asn Ile Leu Gln Thr Gln Lys Ile Met Gln	370		375		380
Glu Asp Arg Gln Ala Val Gln Asp Thr Ile Lys Val Val Ser Asp Val	385		390		395
					400

Lys Ala Gly Asn Phe Ala Val Arg Ile Thr Ala Glu Pro Ala Ser Pro  
 405 410 415  
 Asp Leu Lys Glu Leu Arg Asp Ala Leu Asn Gly Ile Met Asp Tyr Leu  
 420 425 430  
 Gln Glu Ser Val Gly Thr His Met Pro Ser Ile Phe Lys Ile Phe Glu  
 435 440 445  
 Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile Gln Asn Ala Ser Gly  
 450 455 460  
 Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln Glu Ile Gln Lys Met  
 465 470 475 480  
 Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu Ala Asn Asp Ser Ala  
 485 490 495  
 Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys Ala Ser Asn Ser Gln  
 500 505 510  
 His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile Glu Asn Ile Thr Thr  
 515 520 525  
 Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala Met Ile Glu Gln Gly  
 530 535 540  
 Gln Asp Ile Lys Ser Ile Val Glu Ile Ile Arg Asp Ile Ala Asp Gln  
 545 550 555 560  
 Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly  
 565 570 575  
 Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg Lys Leu  
 580 585 590  
 Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile Glu Ala Asn Ile Asn  
 595 600 605  
 Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu Ser Ile Lys Asn Gln  
 610 615 620  
 Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu Arg Ser  
 625 630 635 640  
 Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu Ile Ser  
 645 650 655  
 Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val Asn Lys  
 660 665 670  
 Lys Gln Phe \*  
 675

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 Base pairs

(B) TYPE: Nucleotide

(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(vii) DIRECT SOURCE:

(B) CLONE(S): HPS161

(ix) FEATURES:

(A) NAME/KEY: CDS

(B) POSITION:1..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GTG GCG GTG AAA AAA ATC GTT GTG AGT TGG TGT GTG GCG TTG GCT TTT	48
Val Ala Val Lys Lys Ile Val Val Ser Trp Cys Val Ala Leu Ala Phe	
680 685 690	
TTA AGC GCG GAT TCA GCA CAA GCC AAT AAA GCG ATC AGT AAT GCG GAT	96
Leu Ser Ala Asp Ser Ala Gln Ala Asn Lys Ala Ile Ser Asn Ala Asp	
695 700 705	
TTG ATT AAA GAG ATA AGG GAT TTA AAA AAA ATC ATC AGC GCG CAA AAC	144
Leu Ile Lys Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala Gln Asn	
710 715 720	
ACT GAG ATT AAC AAC TTA AGA AAA GTG CAA GAA GTG TTG TCT GGG CAA	192
Thr Glu Ile Asn Asn Leu Arg Lys Val Gln Glu Val Leu Ser Gly Gln	
725 730 735 740	
TTA GGG GAC ATG CGT AAG GAT ATA TTA AGC ACT AGA GAT TAT TGC ATT	240
Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr Cys Ile	
745 750 755	
AGC TTA AGG CCT TAT ATC TAT AAT TGG CGC TAG	273
Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg *	
760 765	

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 Amino acids

(B) TYPE: Amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

Val Ala Val Lys Lys Ile Val Val Ser Trp Cys Val Ala Leu Ala Phe	
1 5 10 15	
Leu Ser Ala Asp Ser Ala Gln Ala Asn Lys Ala Ile Ser Asn Ala Asp	
20 25 30	
Leu Ile Lys Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala Gln Asn	
35 40 45	

Thr Glu Ile Asn Asn Leu Arg Lys Val Gln Glu Val Leu Ser Gly Gln  
 50 55 60

Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr Cys Ile  
 65 70 75 80

Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg \*

85 90

## (2) INFORMATION FOR SEQ ID NO: 107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS176

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..759

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

ATG TTA GGG AAA AAA AAC GAA GAA GTC TTG ATT GAT GAA AAT TTG GTT	48
Met Leu Gly Lys Lys Asn Glu Glu Val Leu Ile Asp Glu Asn Leu Val	
95 100 105	
GGG GGT GTG ATA GCC CTT GAT AGA TTG GCA AAA CTC AAT AAG GCC AAT	96
Gly Gly Val Ile Ala Leu Asp Arg Leu Ala Lys Leu Asn Lys Ala Asn	
110 115 120	
AGG ACT TTC AAA AGG GCT TTT TAT CTC TCT ATG GCA CTC AAT GTC GCC	144
Arg Thr Phe Lys Arg Ala Phe Tyr Leu Ser Met Ala Leu Asn Val Ala	
125 130 135	
GCT GTA ACG AGT ATT GTG ATG ATG ATG CCT TTG AAG AAA ACG GAT ATA	192
Ala Val Thr Ser Ile Val Met Met Met Pro Leu Lys Lys Thr Asp Ile	
140 145 150 155	
TTT GTT TAT GGC ATT GAT CGA TAC ACA GGA GAA TTT AAA ATT GTC AAA	240
Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Glu Phe Lys Ile Val Lys	
160 165 170	
CGC TCC GAT GCT AGG CAA ATC GTC AAT TCT GAA GCC GTT GTG GAT AGT	288
Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val Val Asp Ser	
175 180 185	
GCA ACT TCA AAA TTT GTA TCA TTG CTG TTT GGT TAT AGC AAA AAT TCT	336
Ala Thr Ser Lys Phe Val Ser Leu Phe Gly Tyr Ser Lys Asn Ser	
190 195 200	
TTG AGG GAT CGC AAG GAT CAA CTA ATG CAG TAT TGC GAT GTG AGT TTC	384
Leu Arg Asp Arg Lys Asp Gln Leu Met Gln Tyr Cys Asp Val Ser Phe	

205	210	215	
CAA ACC CAA GCA ATG AGA ATG TTC AAT GAA AAT ATC AGA CAA TTC GTA Gln Thr Gln Ala Met Arg Met Phe Asn Glu Asn Ile Arg Gln Phe Val 220 225 230 235			432
GAT AAA GTC CGA GCA GAA GCT ATC ATT AGC TCT AAC ATA CAA AGA GAA Asp Lys Val Arg Ala Glu Ala Ile Ile Ser Ser Asn Ile Gln Arg Glu 240 245 250			480
AAA GTC AAA AAT AGT CCC TTA ACG AGA TTA ACA TTT TTC ATT ACC ATC Lys Val Lys Asn Ser Pro Leu Thr Arg Leu Thr Phe Phe Ile Thr Ile 255 260 265			528
AAA ATC ACA CCT GAT ACA ATG GAA AAT TAT GAA TAT ATC ACT AAA AAA Lys Ile Thr Pro Asp Thr Met Glu Asn Tyr Glu Tyr Ile Thr Lys Lys 270 275 280			576
CAA GTA ACT ATT TAT TAT GAT TTT GCT AGA GGT AAC TCT TCT CAA GAA Gln Val Thr Ile Tyr Tyr Asp Phe Ala Arg Gly Asn Ser Ser Gln Glu 285 290 295			624
AAT CTT ATC ATC AAT CCT TTT GGC TTC AAA GTG TTT GAC ATT CAA ATC Asn Leu Ile Ile Asn Pro Phe Gly Phe Lys Val Phe Asp Ile Gln Ile 300 305 310 315			672
ACA GAT TTA CAA AAC GAA CAG ACG GTA AGC GAA ATT TTG AGA AAG ATC Thr Asp Leu Gln Asn Glu Gln Thr Val Ser Glu Ile Leu Arg Lys Ile 320 325 330			720
AGA GAA GTG GAA TCA AAA AAT AAG GCA TTA AAT AAA TAA Arg Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys *			759
335 340			

## (2) INFORMATION FOR SEQ ID NO: 108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

Met	Leu	Gly	Lys	Lys	Asn	Glu	Glu	Val	Leu	Ile	Asp	Glu	Asn	Leu	Val
1				5					10					15	
Gly	Gly	Val	Ile	Ala	Leu	Asp	Arg	Leu	Ala	Lys	Leu	Asn	Lys	Ala	Asn
		20						25					30		
Arg	Thr	Phe	Lys	Arg	Ala	Phe	Tyr	Leu	Ser	Met	Ala	Leu	Asn	Val	Ala
		35					40					45			
Ala	Val	Thr	Ser	Ile	Val	Met	Met	Met	Pro	Leu	Lys	Lys	Thr	Asp	Ile
	50					55				60					
Phe	Val	Tyr	Gly	Ile	Asp	Arg	Tyr	Thr	Gly	Glu	Phe	Lys	Ile	Val	Lys
65				70					75					80	

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Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val Val Asp Ser
      85                      90                      95

Ala Thr Ser Lys Phe Val Ser Leu Leu Phe Gly Tyr Ser Lys Asn Ser
      100                      105                      110

Leu Arg Asp Arg Lys Asp Gln Leu Met Gln Tyr Cys Asp Val Ser Phe
      115                      120                      125

Gln Thr Gln Ala Met Arg Met Phe Asn Glu Asn Ile Arg Gln Phe Val
      130                      135                      140

Asp Lys Val Arg Ala Glu Ala Ile Ile Ser Ser Asn Ile Gln Arg Glu
      145                      150                      155                      160

Lys Val Lys Asn Ser Pro Leu Thr Arg Leu Thr Phe Phe Ile Thr Ile
      165                      170                      175

Lys Ile Thr Pro Asp Thr Met Glu Asn Tyr Glu Tyr Ile Thr Lys Lys
      180                      185                      190

Gln Val Thr Ile Tyr Tyr Asp Phe Ala Arg Gly Asn Ser Ser Gln Glu
      195                      200                      205

Asn Leu Ile Ile Asn Pro Phe Gly Phe Lys Val Phe Asp Ile Gln Ile
      210                      215                      220

Thr Asp Leu Gln Asn Glu Gln Thr Val Ser Glu Ile Leu Arg Lys Ile
      225                      230                      235                      240

Arg Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys *
      245                      250

```

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1245 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS187

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1245

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

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ATG GAG AAA GGA GTT TGG AAT ATG CTT GAC ATA TGG ATA GAT ATG ATA      48
Met Glu Lys Gly Val Trp Asn Met Leu Asp Ile Trp Ile Asp Met Ile
      255                      260                      265

ATT TGT ATT TTT TAT TTG CTC TTT TTT ACG ACT CCT TAC ATT GTA GGC      96

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Ile	Cys	Ile	Phe	Tyr	Leu	Leu	Phe	Phe	Thr	Thr	Pro	Tyr	Ile	Val	Gly	
270					275				280						285	
GAT	ATT	TTG	CAA	TTG	AAA	TTT	ATC	CGC	CAA	AAG	CTC	TGC	GAA	AAA	CCT	144
Asp	Ile	Leu	Gln	Leu	Lys	Phe	Ile	Arg	Gln	Lys	Leu	Cys	Glu	Lys	Pro	
			290						295					300		
GTT	TTA	CTC	CCA	CAA	AAG	GAT	TAT	GAA	GAA	GCG	GGA	AAT	TAT	GCC	ATT	192
Val	Leu	Leu	Pro	Gln	Lys	Asp	Tyr	Glu	Glu	Ala	Gly	Asn	Tyr	Ala	Ile	
			305					310					315			
AGG	AAA	ATG	CAA	TTA	TCC	ATT	ATT	TCT	CAA	ATT	TTA	GAC	GGG	ATA	ATC	240
Arg	Lys	Met	Gln	Leu	Ser	Ile	Ile	Ser	Gln	Ile	Leu	Asp	Gly	Ile	Ile	
		320					325					330				
TTT	GCT	GGG	TGG	GTC	TTT	TTT	GGT	TTG	ACG	CAT	TTA	GAA	GAT	CTC	ACG	288
Phe	Ala	Gly	Trp	Val	Phe	Phe	Gly	Leu	Thr	His	Leu	Glu	Asp	Leu	Thr	
	335				340						345					
CAT	TAT	TTA	AAC	CTT	CCT	GAA	ACG	CTA	GGT	TAC	TTG	GTG	TTT	GCC	TTG	336
His	Tyr	Leu	Asn	Leu	Pro	Glu	Thr	Leu	Gly	Tyr	Leu	Val	Phe	Ala	Leu	
350					355				360						365	
TTG	TTT	TTA	GCG	ATT	CAA	AGC	GTT	TTA	GCT	TTA	CCC	ATT	AGC	TAC	TAC	384
Leu	Phe	Leu	Ala	Ile	Gln	Ser	Val	Leu	Ala	Leu	Pro	Ile	Ser	Tyr	Tyr	
			370					375						380		
ACC	ACG	ATG	CAT	TTG	GAT	AAG	GAA	TTT	GGC	TTT	TCT	AAG	GTG	AGC	TTG	432
Thr	Thr	Met	His	Leu	Asp	Lys	Glu	Phe	Gly	Phe	Ser	Lys	Val	Ser	Leu	
			385					390					395			
TCG	TTG	TTT	TTT	AAG	GAT	TTT	TTC	AAA	GGG	TTA	TCG	CTC	ACT	TTA	AGC	480
Ser	Leu	Phe	Phe	Lys	Asp	Phe	Phe	Lys	Gly	Leu	Ser	Leu	Thr	Leu	Ser	
	400						405					410				
GTG	GGG	TTG	TTG	TTG	ATT	TAC	ACT	CTC	ATT	ATG	ATC	ATT	GAA	CAT	GTG	528
Val	Gly	Leu	Leu	Leu	Ile	Tyr	Thr	Leu	Ile	Met	Ile	Ile	Glu	His	Val	
	415				420					425						
GAA	CAT	TGG	GAG	ATT	AGC	TCG	TTT	TTT	GTC	GTG	TTT	GTT	TTT	ATG	ATC	576
Glu	His	Trp	Glu	Ile	Ser	Ser	Phe	Phe	Val	Val	Phe	Val	Phe	Met	Ile	
430					435				440					445		
TTG	GCT	AAT	CTT	TTT	TAC	CCT	AAA	ATC	GCT	CAG	CTT	TTC	AAC	CAA	TTC	624
Leu	Ala	Asn	Leu	Phe	Tyr	Pro	Lys	Ile	Ala	Gln	Leu	Phe	Asn	Gln	Phe	
			450					455					460			
ACC	CCC	TTG	AAC	AAT	AGG	GAT	TTA	GAG	AGT	CAA	ATT	GAG	GGC	ATG	ATG	672
Thr	Pro	Leu	Asn	Asn	Arg	Asp	Leu	Glu	Ser	Gln	Ile	Glu	Gly	Met	Met	
			465				470					475				
GAT	AAG	GTG	GGT	TTT	AAA	TCT	GAA	GGT	ATC	TTT	GTG	ATG	GAC	GCT	AGC	720
Asp	Lys	Val	Gly	Phe	Lys	Ser	Glu	Gly	Ile	Phe	Val	Met	Asp	Ala	Ser	
	480						485					490				
AAG	AGG	GAC	GGG	CGT	TTG	AAC	GCG	TAT	TTT	GGA	GGC	TTG	GGT	AAA	AAC	768
Lys	Arg	Asp	Gly	Arg	Leu	Asn	Ala	Tyr	Phe	Gly	Gly	Leu	Gly	Lys	Asn	
	495				500						505					

AAG CGG GTG GTG TTG TTT GAC ACT TTG ATC TCT AAA GTT GGG ACA GAA	816
Lys Arg Val Val Leu Phe Asp Thr Leu Ile Ser Lys Val Gly Thr Glu	
510 515 520 525	
GGG CTT TTA GCC ATT TTA GGG CAT GAA TTA GGG CAT TTT AAA AAT AAG	864
Gly Leu Leu Ala Ile Leu Gly His Glu Leu Gly His Phe Lys Asn Lys	
530 535 540	
GAT TTG TTG AAA AGT TTA GGG ATT ATG GGA GGC TTA CTC GCT CTT GTT	912
Asp Leu Leu Lys Ser Leu Gly Ile Met Gly Gly Leu Leu Ala Leu Val	
545 550 555	
TTT GCT CTG ATC GCT CAT TTG CCG CCG TTG GTT TTT GAA GGC TTC AAT	960
Phe Ala Leu Ile Ala His Leu Pro Leu Val Phe Glu Gly Phe Asn	
560 565 570	
GTC TCA CAA ACG CCA GCG AGT TTG ATT GCG ATT TTA CTC TTG TTT TTG	1008
Val Ser Gln Thr Pro Ala Ser Leu Ile Ala Ile Leu Leu Leu Phe Leu	
575 580 585	
CCG GTA TTT TCT TTT TAC GCT ATG CCT TTG ATC GGG TTT TTT AGC CGA	1056
Pro Val Phe Ser Phe Tyr Ala Met Pro Leu Ile Gly Phe Phe Ser Arg	
590 595 600 605	
AAG AAT GAA TAC AAT GCA GAC AAG TTT GGG GCG AGT TTA AGC TCT AAA	1104
Lys Asn Glu Tyr Asn Ala Asp Lys Phe Gly Ala Ser Leu Ser Ser Lys	
610 615 620	
GAG GTT TTA GCC AAA GCG TTA GTG TCT ATT GTG AGT GAG AAT AAA GCG	1152
Glu Val Leu Ala Lys Ala Leu Val Ser Ile Val Ser Glu Asn Lys Ala	
625 630 635	
TTC CCC TAT TCG CAC CCT TTT TAT GTT TTC TTG CAT TTC ACG CAC CCG	1200
Phe Pro Tyr Ser His Pro Phe Tyr Val Phe Leu His Phe Thr His Pro	
640 645 650	
CCC TTA TTA GAG CGC TTG AAA GCT TTG GAT TAT GAA ATT GAA TGA	1245
Pro Leu Leu Glu Arg Leu Lys Ala Leu Asp Tyr Glu Ile Glu *	
655 660 665	

## (2) INFORMATION FOR SEQ ID NO: 110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Met Glu Lys Gly Val Trp Asn Met Leu Asp Ile Trp Ile Asp Met Ile  
1 5 10 15

Ile Cys Ile Phe Tyr Leu Leu Phe Phe Thr Thr Pro Tyr Ile Val Gly  
20 25 30

Asp Ile Leu Gln Leu Lys Phe Ile Arg Gln Lys Leu Cys Glu Lys Pro  
35 40 45

Val Leu Leu Pro Gln Lys Asp Tyr Glu Glu Ala Gly Asn Tyr Ala Ile  
 50 55 60  
 Arg Lys Met Gln Leu Ser Ile Ile Ser Gln Ile Leu Asp Gly Ile Ile  
 65 70 75 80  
 Phe Ala Gly Trp Val Phe Phe Gly Leu Thr His Leu Glu Asp Leu Thr  
 85 90 95  
 His Tyr Leu Asn Leu Pro Glu Thr Leu Gly Tyr Leu Val Phe Ala Leu  
 100 105 110  
 Leu Phe Leu Ala Ile Gln Ser Val Leu Ala Leu Pro Ile Ser Tyr Tyr  
 115 120 125  
 Thr Thr Met His Leu Asp Lys Glu Phe Gly Phe Ser Lys Val Ser Leu  
 130 135 140  
 Ser Leu Phe Phe Lys Asp Phe Phe Lys Gly Leu Ser Leu Thr Leu Ser  
 145 150 155 160  
 Val Gly Leu Leu Leu Ile Tyr Thr Leu Ile Met Ile Ile Glu His Val  
 165 170 175  
 Glu His Trp Glu Ile Ser Ser Phe Phe Val Val Phe Val Phe Met Ile  
 180 185 190  
 Leu Ala Asn Leu Phe Tyr Pro Lys Ile Ala Gln Leu Phe Asn Gln Phe  
 195 200 205  
 Thr Pro Leu Asn Asn Arg Asp Leu Glu Ser Gln Ile Glu Gly Met Met  
 210 215 220  
 Asp Lys Val Gly Phe Lys Ser Glu Gly Ile Phe Val Met Asp Ala Ser  
 225 230 235 240  
 Lys Arg Asp Gly Arg Leu Asn Ala Tyr Phe Gly Gly Leu Gly Lys Asn  
 245 250 255  
 Lys Arg Val Val Leu Phe Asp Thr Leu Ile Ser Lys Val Gly Thr Glu  
 260 265 270  
 Gly Leu Leu Ala Ile Leu Gly His Glu Leu Gly His Phe Lys Asn Lys  
 275 280 285  
 Asp Leu Leu Lys Ser Leu Gly Ile Met Gly Gly Leu Leu Ala Leu Val  
 290 295 300  
 Phe Ala Leu Ile Ala His Leu Pro Pro Leu Val Phe Glu Gly Phe Asn  
 305 310 315 320  
 Val Ser Gln Thr Pro Ala Ser Leu Ile Ala Ile Leu Leu Leu Phe Leu  
 325 330 335  
 Pro Val Phe Ser Phe Tyr Ala Met Pro Leu Ile Gly Phe Phe Ser Arg  
 340 345 350  
 Lys Asn Glu Tyr Asn Ala Asp Lys Phe Gly Ala Ser Leu Ser Ser Lys

355	360	365
Glu Val Leu Ala Lys Ala Leu Val Ser Ile Val Ser Glu Asn Lys Ala		
370	375	380
Phe Pro Tyr Ser His Pro Phe Tyr Val Phe Leu His Phe Thr His Pro		
385	390	395
Pro Leu Leu Glu Arg Leu Lys Ala Leu Asp Tyr Glu Ile Glu *		
405	410	415

## (2) INFORMATION FOR SEQ ID NO: 111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

(B) CLONE(S): HPS189

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION:1..1566

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

ATG AAA AAC ATT TAT CTT GAT GTG AAA GCC AGC ATT GAA AAT CTC CAA	48
Met Lys Asn Ile Tyr Leu Asp Val Lys Ala Ser Ile Glu Asn Leu Gln	
420	425
AAT ATT TTT AAA AAC ACT GAT AAT GAA AAT GAA AGA CTA AAA AAA TTC	96
Asn Ile Phe Lys Asn Thr Asp Asn Glu Asn Glu Arg Leu Lys Lys Phe	
435	440
AAC CAA GAA GCG TTG GAG GTG TTT CAA AAA TTA GAG CGT GAA AGT TTA	144
Asn Gln Glu Ala Leu Glu Val Phe Gln Lys Leu Glu Arg Glu Ser Leu	
450	455
AAA GAG CTT GAA AGC TTA AAA AAT AAT GAG GAG TGG GAA AAT TTT ACT	192
Lys Glu Leu Glu Ser Leu Lys Asn Asn Glu Glu Trp Glu Asn Phe Thr	
465	470
ATC GCT TTT TAT GGG GAA ACC GGT GCG GGG AAA TCA ACC TTC ATT GAA	240
Ile Ala Phe Tyr Gly Glu Thr Gly Ala Gly Lys Ser Thr Phe Ile Glu	
480	485
TGT TTG AGA ATG TTT TTT AAA GAA CAA AGT AAA GTA GTT CAA CAA GAA	288
Cys Leu Arg Met Phe Phe Lys Glu Gln Ser Lys Val Val Gln Gln Glu	
500	505
CGA TTC AAG CGG CTT TAT TCC AAT TAC CAA AAC AAC TAT CAA AAT GAT	336
Arg Phe Lys Arg Leu Tyr Ser Asn Tyr Gln Asn Asn Tyr Gln Asn Asp	
515	520

GAA TGC AAA AAG CAA GCT ATT TTA AAC GAA CTT CAT TCA TTG CAA GAT Glu Cys Lys Lys Gln Ala Ile Leu Asn Glu Leu His Ser Leu Gln Asp 530 535 540	384
GGA GCG ATC ATA GGC GAT GGG AGG AGC GAT TTC ACT TTA AAA ACA CGA Gly Ala Ile Ile Gly Asp Gly Arg Ser Asp Phe Thr Leu Lys Thr Arg 545 550 555	432
TCT TAT TCT TTC CAA TAC AAC CAT CAA AAC TTT ACT TTG CTT GAT GTT Ser Tyr Ser Phe Gln Tyr Asn His Gln Asn Phe Thr Leu Leu Asp Val 560 565 570 575	480
CCA GGG ATA GAA GGC GAC GAA AAA AAA GTG ATC GAT CAG ATT TCT AAC Pro Gly Ile Glu Gly Asp Glu Lys Lys Val Ile Asp Gln Ile Ser Asn 580 585 590	528
GCA ACG CAA AAA GCC CAT GCT ATT TTT TAT GTT ACC AAA ACG CCT AAT Ala Thr Gln Lys Ala His Ala Ile Phe Tyr Val Thr Lys Thr Pro Asn 595 600 605	576
CCT CCG CAA AAA GGA GAA GAG AAA AAA GAA GGG ACG ATT GAA AAA ATC Pro Pro Gln Lys Gly Glu Glu Lys Lys Glu Gly Thr Ile Glu Lys Ile 610 615 620	624
CAA AAA CAA CTT GAT TCG CAA ACA GAG GTA TGG ACG ATT TTT AAC AAA Gln Lys Gln Leu Asp Ser Gln Thr Glu Val Trp Thr Ile Phe Asn Lys 625 630 635	672
CCG ATT AAC AAC CCA AGA GCT TTC AAA GAT GGG CTT ATT GAT GGA AGC Pro Ile Asn Asn Pro Arg Ala Phe Lys Asp Gly Leu Ile Asp Gly Ser 640 645 650 655	720
GAA AAA GAA AGC TTA AAA ATT TTA AAT AAA GAA ATG AAA AAC ATT TTA Glu Lys Glu Ser Leu Lys Ile Leu Asn Lys Glu Met Lys Asn Ile Leu 660 665 670	768
GGC AAA CAC TAC AAG GGC TAT AAA GCA GTG AGC GCC CAA GTG GCT TTT Gly Lys His Tyr Lys Gly Tyr Lys Ala Val Ser Ala Gln Val Ala Phe 675 680 685	816
TAT GGT CTT TCA TCG GCT TTG ATC CCA GGG ACT GAT TTT GAT AAA AAC Tyr Gly Leu Ser Ser Ala Leu Ile Leu Pro Gly Thr Asp Phe Asp Lys Asn 690 695 700	864
AAA CAA AAA TTT TTA AAA GAT TTT AAA GCA AGA GAA TTA TTG TAT CAA Lys Gln Lys Phe Leu Lys Asp Phe Lys Ala Arg Glu Leu Leu Tyr Gln 705 710 715	912
TCC CAT TTC CAA CAA TTA GGA GAA TTT ATA GCC GAA GAG CTT ATT AAA Ser His Phe Gln Gln Leu Gly Glu Phe Ile Ala Glu Glu Leu Ile Lys 720 725 730 735	960
AAC TCG CGT GCC AAA ATC ATT CAA TCA AAC TGC AAT AAA GCC TTA AAA Asn Ser Arg Ala Lys Ile Ile Gln Ser Asn Cys Asn Lys Ala Leu Lys 740 745 750	1008
GTG GTA GAA CAA TTG CAA AAG GCG ATC GAA ATT ACG ATT GAA AAA CGG Val Val Glu Gln Leu Gln Lys Ala Ile Glu Ile Thr Ile Glu Lys Arg 755 760 765	1056

ATC GAT CCA ATG ATT AAA GAA GCA CAA GAA TAC CAA CAC GAA GCC CGC Ile Asp Pro Met Ile Lys Glu Ala Gln Glu Tyr Gln His Glu Ala Arg 770 775 780	1104
TAT AAT CTG GAT CGT TCT ACA GAT AAA TTT ATA TTA AAT TTA ACC AAT Tyr Asn Leu Asp Arg Ser Thr Asp Lys Phe Ile Leu Asn Leu Thr Asn 785 790 795	1152
TCA GCG TTC TAC GAA ATC GAT CAA TTC AAA TCT GAC TTG AGA GAA AAA Ser Ala Phe Tyr Glu Ile Asp Gln Phe Lys Ser Asp Leu Arg Glu Lys 800 805 810 815	1200
ATG TAT GCG CAT ATT AAC AAA AAT ATT GAA GAT GAG GAA TGT AAA GAA Met Tyr Ala His Ile Asn Lys Asn Ile Glu Asp Glu Glu Cys Lys Glu 820 825 830	1248
ATT TTT AAA AAT GAA CTC ATT CAA GGA ATT GAA ACA TTG CAT GAA GAC Ile Phe Lys Asn Glu Leu Ile Gln Gly Ile Glu Thr Leu His Glu Asp 835 840 845	1296
ATA AAA TGG CGG TTT AGA GAA TGT GAG AAA CGA TTT GAT GGA GAG ATA Ile Lys Trp Arg Phe Arg Glu Cys Glu Lys Arg Phe Asp Gly Glu Ile 850 855 860	1344
AAA GAA GCT ATT AAA CAA CTT GAA TAC AGA ATT AAA GAT TCT CTA GCA Lys Glu Ala Ile Lys Gln Leu Glu Tyr Arg Ile Lys Asp Ser Leu Ala 865 870 875	1392
ATG TTA GAG CGC ATC AGT ATT GAT AGA GAC TTT AAT CTT AAT TTT GAT Met Leu Glu Arg Ile Ser Ile Asp Arg Asp Phe Asn Leu Asn Phe Asp 880 885 890 895	1440
ACT GAT AGC GGT ATT GAT GGA ACA AAA TTA GCC ACT TCA ATA GGA GGT Thr Asp Ser Gly Ile Asp Gly Thr Lys Leu Ala Thr Ser Ile Gly Gly 900 905 910	1488
TTG GGT TTG CTT GGG ATA TTT AAC GCT TGG AAT CCT ATG GGT TGG CTT Leu Gly Leu Leu Gly Ile Phe Asn Ala Trp Asn Pro Met Gly Trp Leu 915 920 925	1536
GCT CTG ACC GCA GGA TTA TTG CAG GAT TAG Ala Leu Thr Ala Gly Leu Leu Gln Asp * 930 935	1566

## (2) INFORMATION FOR SEQ ID NO: 112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Met	Lys	Asn	Ile	Tyr	Leu	Asp	Val	Lys	Ala	Ser	Ile	Glu	Asn	Leu	Gln
1					5				10					15	

Asn Ile Phe Lys Asn Thr Asp Asn Glu Asn Glu Arg Leu Lys Lys Phe  
 20 25 30  
 Asn Gln Glu Ala Leu Glu Val Phe Gln Lys Leu Glu Arg Glu Ser Leu  
 35 40 45  
 Lys Glu Leu Glu Ser Leu Lys Asn Asn Glu Glu Trp Glu Asn Phe Thr  
 50 55 60  
 Ile Ala Phe Tyr Gly Glu Thr Gly Ala Gly Lys Ser Thr Phe Ile Glu  
 65 70 75 80  
 Cys Leu Arg Met Phe Phe Lys Glu Gln Ser Lys Val Val Gln Gln Glu  
 85 90 95  
 Arg Phe Lys Arg Leu Tyr Ser Asn Tyr Gln Asn Asn Tyr Gln Asn Asp  
 100 105 110  
 Glu Cys Lys Lys Gln Ala Ile Leu Asn Glu Leu His Ser Leu Gln Asp  
 115 120 125  
 Gly Ala Ile Ile Gly Asp Gly Arg Ser Asp Phe Thr Leu Lys Thr Arg  
 130 135 140  
 Ser Tyr Ser Phe Gln Tyr Asn His Gln Asn Phe Thr Leu Leu Asp Val  
 145 150 155 160  
 Pro Gly Ile Glu Gly Asp Glu Lys Lys Val Ile Asp Gln Ile Ser Asn  
 165 170 175  
 Ala Thr Gln Lys Ala His Ala Ile Phe Tyr Val Thr Lys Thr Pro Asn  
 180 185 190  
 Pro Pro Gln Lys Gly Glu Glu Lys Lys Glu Gly Thr Ile Glu Lys Ile  
 195 200 205  
 Gln Lys Gln Leu Asp Ser Gln Thr Glu Val Trp Thr Ile Phe Asn Lys  
 210 215 220  
 Pro Ile Asn Asn Pro Arg Ala Phe Lys Asp Gly Leu Ile Asp Gly Ser  
 225 230 235 240  
 Glu Lys Glu Ser Leu Lys Ile Leu Asn Lys Glu Met Lys Asn Ile Leu  
 245 250 255  
 Gly Lys His Tyr Lys Gly Tyr Lys Ala Val Ser Ala Gln Val Ala Phe  
 260 265 270  
 Tyr Gly Leu Ser Ser Ala Leu Ile Pro Gly Thr Asp Phe Asp Lys Asn  
 275 280 285  
 Lys Gln Lys Phe Leu Lys Asp Phe Lys Ala Arg Glu Leu Leu Tyr Gln  
 290 295 300  
 Ser His Phe Gln Gln Leu Gly Glu Phe Ile Ala Glu Glu Leu Ile Lys  
 305 310 315 320  
 Asn Ser Arg Ala Lys Ile Ile Gln Ser Asn Cys Asn Lys Ala Leu Lys  
 325 330 335

Val Val Glu Gln Leu Gln Lys Ala Ile Glu Ile Thr Ile Glu Lys Arg  
                   340                  345                  350  
 Ile Asp Pro Met Ile Lys Glu Ala Gln Glu Tyr Gln His Glu Ala Arg  
                   355                  360                  365  
 Tyr Asn Leu Asp Arg Ser Thr Asp Lys Phe Ile Leu Asn Leu Thr Asn  
                   370                  375                  380  
 Ser Ala Phe Tyr Glu Ile Asp Gln Phe Lys Ser Asp Leu Arg Glu Lys  
                   385                  390                  395                  400  
 Met Tyr Ala His Ile Asn Lys Asn Ile Glu Asp Glu Glu Cys Lys Glu  
                   405                  410                  415  
 Ile Phe Lys Asn Glu Leu Ile Gln Gly Ile Glu Thr Leu His Glu Asp  
                   420                  425                  430  
 Ile Lys Trp Arg Phe Arg Glu Cys Glu Lys Arg Phe Asp Gly Glu Ile  
                   435                  440                  445  
 Lys Glu Ala Ile Lys Gln Leu Glu Tyr Arg Ile Lys Asp Ser Leu Ala  
                   450                  455                  460  
 Met Leu Glu Arg Ile Ser Ile Asp Arg Asp Phe Asn Leu Asn Phe Asp  
                   465                  470                  475                  480  
 Thr Asp Ser Gly Ile Asp Gly Thr Lys Leu Ala Thr Ser Ile Gly Gly  
                   485                  490                  495  
 Leu Gly Leu Leu Gly Ile Phe Asn Ala Trp Asn Pro Met Gly Trp Leu  
                   500                  505                  510  
 Ala Leu Thr Ala Gly Leu Leu Gln Asp \*  
                   515                  520

## (2) INFORMATION FOR SEQ ID NO: 113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

## (vii) DIRECT SOURCE:

- (B) CLONE(S): HPS191

## (ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..1782

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATG AAA GCT ATA AAA ATA CTT TTT ATA ATG ACA CTC AGT TTA AAC GCT  
 Met Lys Ala Ile Lys Ile Leu Phe Ile Met Thr Leu Ser Leu Asn Ala



525					530					535						
ATC Ile	AGC Ser	GTG Val	AAT Asn	AGG Arg	GCG Ala	TTG Leu	TTT Phe	GAT Asp	TTA Leu	AAA Lys	GAT Asp	TCG Ser	CAA Gln	TTA Leu	AAA Lys	96
540					545					550						
GGG Gly	GAA Glu	TTA Leu	ACG Thr	CCA Pro	AAA Lys	ATA Ile	GTG Val	AAT Asn	TTT Phe	GGG Gly	GGT Gly	TAT Tyr	AAA Lys	AGC Ser	AGC Ser	144
555					560					565					570	
ACT Thr	GAA Glu	GAG Glu	TGG Trp	GGG Gly	GCT Ala	ACG Thr	GCT Ala	TTA Leu	AAC Asn	TAT Tyr	ATC Ile	AAT Asn	GCG Ala	GCT Ala	AAT Asn	192
575					580					585						
GGC Gly	GAT Asp	GCG Ala	AAA Lys	AAA Lys	TTC Phe	AGC Ser	ACT Thr	CTA Leu	GTG Val	GAA Glu	AAA Lys	ATG Met	CGT Arg	TTT Phe	AAC Asn	240
590					595					600						
TCC Ser	GGT Gly	ATA Ile	TTG Leu	GGG Gly	AAT Asn	TTA Leu	AGA Arg	GTG Val	CAT His	GCA Ala	CGT Arg	TTG Leu	AGG Arg	CAA Gln	GCC Ala	288
605					610					615						
CTA Leu	AAA Lys	TTG Leu	CAA Gln	AAG Lys	AAT Asn	TTG Leu	AAA Lys	TAT Tyr	TGC Cys	CTT Leu	AAA Lys	ATC Ile	ATC Ile	GCT Ala	AGG Arg	336
620					625					630						
GAT Asp	TCT Ser	TTT Phe	TAT Tyr	AGC Ser	TAC Tyr	CGC Arg	ACC Thr	GGT Gly	ATT Ile	TAT Tyr	ATC Ile	CCC Pro	TTA Leu	GGC Gly	ATT Ile	384
635					640					645					650	
TCT Ser	TTA Leu	AAA Lys	GAT Asp	CAA Gln	AAA Lys	ACG Thr	GCT Ala	CAA Gln	AAA Lys	ATG Met	CTC Leu	GCT Ala	GAT Asp	TTG Leu	AGC Ser	432
655					660					665						
GTG Val	GTA Val	GGG Gly	GCG Ala	TAT Tyr	CTT Leu	AAA Lys	AAA Lys	CAA Gln	CAA Gln	GAG Glu	AAT Asn	GAA Glu	AAG Lys	GCT Ala	CAA Gln	480
670					675					680						
AGC Ser	CCT Pro	TAT Tyr	TAC Tyr	AGA Arg	AAC Asn	AAC Asn	AAC Asn	TAT Tyr	TAC Tyr	AAC Asn	TCT Ser	TAC Tyr	TAT Tyr	AGC Ser	CCT Pro	528
685					690					695						
TAT Tyr	TAC Tyr	GGA Gly	ATG Met	TAT Tyr	GGT Gly	ATG Met	TAT Tyr	GGC Gly	ATG Met	GGC Gly	ATG Met	TAT Tyr	GGA Gly	ATG Met	TAT Tyr	576
700					705					710						
GGC Gly	ATG Met	GGC Gly	ATG Met	TAT Tyr	GAT Asp	TTT Phe	TAT Tyr	GAC Asp	TTT Phe	TAT Tyr	GAT Asp	GGC Gly	ATG Met	TAT Tyr	GGA Gly	624
715					720					725					730	
TTC Phe	TAC Tyr	CCT Pro	AAC Asn	ATG Met	TTT Phe	TTC Phe	ATG Met	ATG Met	CAA Gln	GTT Val	CAA Gln	GAT Asp	TAC Tyr	TTG Leu	ATG Met	672
735					740					745						
TTA Leu	GAA Glu	AAT Asn	TAC Tyr	ATG Met	TAT Tyr	GCG Ala	CTC Leu	GAT Asp	CAA Gln	GAA Glu	GAG Glu	ATT Ile	TTA Leu	GAT Asp	CAT His	720
750					755					760						
GAC	GCT	TCT	ACT	GAC	CAA	CTT	GAT	ACG	CCT	ACT	GAT	GAT	GAC	AAA	GAC	768

Asp	Ala	Ser	Thr	Asp	Gln	Leu	Asp	Thr	Pro	Thr	Asp	Asp	Asp	Lys	Asp	
		765					770				775					
GAT	AAA	GAC	GAT	AAA	TCC	TTA	CAG	CAG	GCA	AAT	CTT	ATG	AAC	TTT	TAT	816
Asp	Lys	Asp	Asp	Lys	Ser	Leu	Gln	Gln	Ala	Asn	Leu	Met	Asn	Phe	Tyr	
	780					785					790					
CGT	GAT	CCC	AAA	TTC	AGC	AAA	GGC	ATT	CAA	ACC	AAC	CGC	TTG	AAT	AGC	864
Arg	Asp	Pro	Lys	Phe	Ser	Lys	Gly	Ile	Gln	Thr	Asn	Arg	Leu	Asn	Ser	
	795				800					805					810	
GCT	TTA	GTC	AAT	TTA	GAC	AAC	AGT	CGC	ATG	CTC	AAA	GAC	AAT	TCG	CTT	912
Ala	Leu	Val	Asn	Leu	Asp	Asn	Ser	Arg	Met	Leu	Lys	Asp	Asn	Ser	Leu	
				815					820					825		
TTC	CAC	ACT	AAA	GCC	ATG	CCC	ACT	AAA	AGC	GTG	GAT	GCG	ATA	ACT	TCT	960
Phe	His	Thr	Lys	Ala	Met	Pro	Thr	Lys	Ser	Val	Asp	Ala	Ile	Thr	Ser	
			830					835					840			
CAA	GCC	AAA	GAG	CTT	AAC	CAT	TTA	GTG	GGG	CAA	ATC	AAA	GAA	ATG	AAG	1008
Gln	Ala	Lys	Glu	Leu	Asn	His	Leu	Val	Gly	Gln	Ile	Lys	Glu	Met	Lys	
		845					850					855				
CAA	GAC	GGG	GCG	AGT	CCT	AGT	AAG	ATT	GAT	TCA	GTT	GTC	AAT	AAA	GCT	1056
Gln	Asp	Gly	Ala	Ser	Pro	Ser	Lys	Ile	Asp	Ser	Val	Val	Asn	Lys	Ala	
	860					865					870					
ATG	GAA	GTG	AGG	GAC	AAG	CTA	GAC	AAT	AAT	CTC	AAC	CAA	CTA	GAC	AAT	1104
Met	Glu	Val	Arg	Asp	Lys	Leu	Asp	Asn	Asn	Leu	Asn	Gln	Leu	Asp	Asn	
	875				880					885					890	
GAC	TTA	AAA	GAT	CAA	AAA	GGG	CTT	TCA	AGC	GAG	CAA	CAA	GCT	CAA	GTG	1152
Asp	Leu	Lys	Asp	Gln	Lys	Gly	Leu	Ser	Ser	Glu	Gln	Gln	Ala	Gln	Val	
				895					900					905		
GAT	AAA	GCC	CTA	GAC	AGC	GTG	CAA	CAA	TTA	AGC	CAT	AGC	AGC	GAT	GTG	1200
Asp	Lys	Ala	Leu	Asp	Ser	Val	Gln	Gln	Leu	Ser	His	Ser	Ser	Asp	Val	
		910					915						920			
GTG	GGG	AAT	TAT	TTA	GAC	GGG	AGT	TTG	AAA	ATT	GAT	GGC	GAT	GAT	AGA	1248
Val	Gly	Asn	Tyr	Leu	Asp	Gly	Ser	Leu	Lys	Ile	Asp	Gly	Asp	Asp	Arg	
		925					930					935				
GAT	GAT	TTG	AAT	GAT	GCG	ATG	AAT	AAC	CCT	ATG	CAA	CAA	CCC	GTG	CAA	1296
Asp	Asp	Leu	Asn	Asp	Ala	Met	Asn	Asn	Pro	Met	Gln	Gln	Pro	Val	Gln	
	940					945					950					
CAA	ACG	CCT	ACT	AGC	AAC	ATG	GCC	GAC	ACC	CAT	GCA	AAT	GAC	AGC	AAG	1344
Gln	Thr	Pro	Thr	Ser	Asn	Met	Ala	Asp	Thr	His	Ala	Asn	Asp	Ser	Lys	
	955				960					965					970	
GAT	CAA	GGG	AGT	AAC	GCG	CTC	ATA	AAC	CCT	AAC	AGC	GCC	ACT	AAC	GCC	1392
Asp	Gln	Gly	Ser	Asn	Ala	Leu	Ile	Asn	Pro	Asn	Ser	Ala	Thr	Asn	Ala	
				975					980					985		
GAC	GAC	ACT	CAC	ACT	GAC	GAT	ACT	CAC	ACT	GAC	ACT	AAC	ACC	ACA	AAC	1440
Asp	Asp	Thr	His	Thr	Asp	Asp	Thr	His	Thr	Asp	Thr	Asn	Thr	Thr	Asn	
			990					995					1000			

GAT GCT AGC ACC ACT GAC ACC CCC ACT GAC GAT AAA GAT GCT AGC GGC Asp Ala Ser Thr Thr Asp Thr Pro Thr Asp Asp Lys Asp Ala Ser Gly 1005 1010 1015	1488
TTG AAC AAT ACC GGC GAT ATG AAT AAC ACG GAT ACC GGC AAC ACG GAC Leu Asn Asn Thr Gly Asp Met Asn Asn Thr Asp Thr Gly Asn Thr Asp 1020 1025 1030	1536
ACC GGC AAT ACG GAT ACC GGT AAC ACT GAT GAT ATG AGC AAC ATG AAC Thr Gly Asn Thr Asp Thr Gly Asn Thr Asp Asp Met Ser Asn Met Asn 1035 1040 1045 1050	1584
AAC GGC AAC GAT GAT ACG GGT AAC GCT AAT GAC GAC ATG AGC AAC GGC Asn Gly Asn Asp Asp Thr Gly Asn Ala Asn Asp Asp Met Ser Asn Gly 1055 1060 1065	1632
AAC GAC ATG GGC GAT GAT TTG AAC AAC GCG AAC GAT ATG AAC GAC GAC Asn Asp Met Gly Asp Asp Leu Asn Asn Ala Asn Asp Met Asn Asp Asp 1070 1075 1080	1680
ATG GGT AAT GGC AAC GAT GAC ATG GGC GAT ATG GGG GAT ATG AAC GAC Met Gly Asn Gly Asn Asp Asp Met Gly Asp Met Gly Asp Met Asn Asp 1085 1090 1095	1728
GAT ATG GGT GGC GAT ATG GGA GAC ATG GGG GAT ATG GGC GAT ATG GGG Asp Met Gly Gly Asp Met Gly Asp Met Gly Asp Met Gly Asp Met Gly 1100 1105 1110	1776
AAT TGA Asn * 1115	1782

## (2) INFORMATION FOR SEQ ID NO: 114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 Amino acids
- (B) TYPE: Amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Met Lys Ala Ile Lys Ile Leu Phe Ile Met Thr Leu Ser Leu Asn Ala 1 5 10 15
Ile Ser Val Asn Arg Ala Leu Phe Asp Leu Lys Asp Ser Gln Leu Lys 20 25 30
Gly Glu Leu Thr Pro Lys Ile Val Asn Phe Gly Gly Tyr Lys Ser Ser 35 40 45
Thr Glu Glu Trp Gly Ala Thr Ala Leu Asn Tyr Ile Asn Ala Ala Asn 50 55 60
Gly Asp Ala Lys Lys Phe Ser Thr Leu Val Glu Lys Met Arg Phe Asn 65 70 75 80
Ser Gly Ile Leu Gly Asn Leu Arg Val His Ala Arg Leu Arg Gln Ala

85	90	95
Leu Lys Leu Gln Lys Asn Leu Lys Tyr Cys Leu Lys Ile Ile Ala Arg		
100	105	110
Asp Ser Phe Tyr Ser Tyr Arg Thr Gly Ile Tyr Ile Pro Leu Gly Ile		
115	120	125
Ser Leu Lys Asp Gln Lys Thr Ala Gln Lys Met Leu Ala Asp Leu Ser		
130	135	140
Val Val Gly Ala Tyr Leu Lys Lys Gln Gln Glu Asn Glu Lys Ala Gln		
145	150	155
Ser Pro Tyr Tyr Arg Asn Asn Asn Tyr Tyr Asn Ser Tyr Tyr Ser Pro		
165	170	175
Tyr Tyr Gly Met Tyr Gly Met Tyr Gly Met Gly Met Tyr Gly Met Tyr		
180	185	190
Gly Met Gly Met Tyr Asp Phe Tyr Asp Phe Tyr Asp Gly Met Tyr Gly		
195	200	205
Phe Tyr Pro Asn Met Phe Phe Met Met Gln Val Gln Asp Tyr Leu Met		
210	215	220
Leu Glu Asn Tyr Met Tyr Ala Leu Asp Gln Glu Glu Ile Leu Asp His		
225	230	235
Asp Ala Ser Thr Asp Gln Leu Asp Thr Pro Thr Asp Asp Asp Lys Asp		
245	250	255
Asp Lys Asp Asp Lys Ser Leu Gln Gln Ala Asn Leu Met Asn Phe Tyr		
260	265	270
Arg Asp Pro Lys Phe Ser Lys Gly Ile Gln Thr Asn Arg Leu Asn Ser		
275	280	285
Ala Leu Val Asn Leu Asp Asn Ser Arg Met Leu Lys Asp Asn Ser Leu		
290	295	300
Phe His Thr Lys Ala Met Pro Thr Lys Ser Val Asp Ala Ile Thr Ser		
305	310	315
Gln Ala Lys Glu Leu Asn His Leu Val Gly Gln Ile Lys Glu Met Lys		
325	330	335
Gln Asp Gly Ala Ser Pro Ser Lys Ile Asp Ser Val Val Asn Lys Ala		
340	345	350
Met Glu Val Arg Asp Lys Leu Asp Asn Asn Leu Asn Gln Leu Asp Asn		
355	360	365
Asp Leu Lys Asp Gln Lys Gly Leu Ser Ser Glu Gln Gln Ala Gln Val		
370	375	380
Asp Lys Ala Leu Asp Ser Val Gln Gln Leu Ser His Ser Ser Asp Val		
385	390	395
		400

Val Gly Asn Tyr Leu Asp Gly Ser Leu Lys Ile Asp Gly Asp Asp Arg  
 405 410 415  
 Asp Asp Leu Asn Asp Ala Met Asn Asn Pro Met Gln Gln Pro Val Gln  
 420 425 430  
 Gln Thr Pro Thr Ser Asn Met Ala Asp Thr His Ala Asn Asp Ser Lys  
 435 440 445  
 Asp Gln Gly Ser Asn Ala Leu Ile Asn Pro Asn Ser Ala Thr Asn Ala  
 450 455 460  
 Asp Asp Thr His Thr Asp Asp Thr His Thr Asp Thr Asn Thr Thr Asn  
 465 470 475 480  
 Asp Ala Ser Thr Thr Asp Thr Pro Thr Asp Asp Lys Asp Ala Ser Gly  
 485 490 495  
 Leu Asn Asn Thr Gly Asp Met Asn Asn Thr Asp Thr Gly Asn Thr Asp  
 500 505 510  
 Thr Gly Asn Thr Asp Thr Gly Asn Thr Asp Asp Met Ser Asn Met Asn  
 515 520 525  
 Asn Gly Asn Asp Asp Thr Gly Asn Ala Asn Asp Asp Met Ser Asn Gly  
 530 535 540  
 Asn Asp Met Gly Asp Asp Leu Asn Asn Ala Asn Asp Met Asn Asp Asp  
 545 550 555 560  
 Met Gly Asn Gly Asn Asp Asp Met Gly Asp Met Gly Asp Met Asn Asp  
 565 570 575  
 Asp Met Gly Gly Asp Met Gly Asp Met Gly Asp Met Gly Asp Met Gly  
 580 585 590

Asn \*